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**FIGURE 88**

MAAASRSASGWallLLLVALWQQAAGSGVFLQLQEFINERGVLASGRPCPEGCRTFFRVCLK  
HFQAVVSPGPCTFGTVSTPVLGTNSFAVRDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG  
DDLRLPEALPPDALISKIAIQGSLAVGQNWLLDEQTSSTLRLRYSYRVICSDNYGDNCSRLCK  
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQOPICLSGCHEQNGYCSKPAECLCRPGWQGRICNE  
CIPHNGCRHGTCSTPQWQCTCDEGWGGLFCDQDLNYCTHHSPCKNGATCSNSGQRSYTCTCRPG  
YTGVDCELELSECDSNPCRNNGGSKDQEDGYHCLCPPGYGLHCEHSTLSCADSPCFNGGSCR  
ERNQGANAYACECPPNFTGSNCEKKVDRCTSNPCANGGQCLNRGPSRMCRCRPGFTGTYCELHV  
SDCARNPCAAGGTCHDLENGLMCTCPAGFSGRRCVVRTSIDACASSPCFNATCTYDLSTDTF  
VCNCPYGFVGSRCFFVGLPPSFPWVAVSLGVGLAVLLVLLGMVAVAVRQLRLRRPDDGSREA  
MNNLSDFQKDNLI PAAQLKNTNQKKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPEGK  
FPHSDKSLGEKAPLRLHSEKPECRISAICSPRDSMYQSVCLISEERNECVIATEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

**Glycosaminoglycan attachment site.**

amino acids 96-100

**Tyrosine kinase phosphorylation site.**

amino acids 340-347

**N-myristoylation sites.**

amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631

**Amidation site.**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

**EGF-like domain cysteine pattern signature.**

amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,  
388-400, 426-438, 464-476, 506-518

**Calcium-binding EGF-like:**

amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,  
449-470

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**FIGURE 89**

GTCTCCGCGTACAGGAACTTCAGCACCCACAGGCGGACAGCGCTCCCCTCTACCTGGAGAC  
TTGACTCCC GCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCAGC  
CGCCCACTCCCGGCCCTCTCCCGCCCCACCCACCCTCCTGGCTCTTCTGTTTTTACTCC  
TCTTTTTCATTATAACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCC  
GAGCGTGGAAGAATGGGGTTCCTCGGGACCGGCCTTGGAATTCTGGTGTTAGTGCTCCCGATT  
CAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAATCTCTACATAATAGAGAATTAAGTGCA  
GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAATAAACATATCCT  
CCAGAAAACAAGCCAGGTCAGAGCAACTATCTTTTGTGTGATACTTGAACCTGCTAAAGGCA  
ATAACAGAAAAGGAAAAAATTGAGAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT  
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT  
ACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC  
AGAGCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA  
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAA  
AATTATGAGGAGGATCCCAATAAGCCCCACAAGCTGGACTGAGAATCAGGCTGAAAAAATACCA  
GAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA  
GTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC  
AACTTTGAGGAACCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTAGAA  
AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG  
ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGAT  
GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAATGCTACTGACAATATAAGCAAG  
CTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
AAGATGGAAGGAATATGGAAGCTTGAAGGATTCACAAAAAGATGATACTCCAACCCAGGA  
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGCCATCAGAAAAAATATT  
GAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAGATTATGACCTTTCAAGATGAGA  
GACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
GAGGCCATCAAGCGCATTATATGACAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAAC  
TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAAATTTTTTGACCC  
AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGC  
TTTCTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAATAAAAAAAAAA  
AAA

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**FIGURE 90**

MGFLGTGTWILVLVLP IQAFPPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKTEKERQSISSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVT PMAAIQDGLAKGENDETVSNT  
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEEA AKMEK  
EYGLKDDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHKGNKEDYDL SKMRDFIN  
KQADAYVEKGILDKEEAEAIKRIYSSI

**Important features:****N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

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**FIGURE 91**

TGCATCAGTGCCCAGGCCAAGCCCAGGAGTTGACATTTCTCTGCCCAGGCCATGGGCCTCACCCCT  
GCTCTTGCTGCTGCTCCTCGGGACTAGAAGGTCAGGGCATAGTTGGCAGCCTCCCTGAGGTGCT  
GCAGGCACCCGTGGGAAGCTCCATTTCTGGTGCAGTGCCACTACAGGCTCCAGGATGTCAAAGC  
TCAGAAGGTGTGGTGCCGTTCTTGCCGGAGGGGTGCCAGCCCCCTGGTGTCTCAGCTGTGGA  
TCGCAGAGCTCCAGCGGGCAGGCGTACGTTTCTCACAGACCTGGGTGGGGCCTGCTGCAGGT  
GGAAATGGTTACCTGCGAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGGCCAG  
GGGGCCCCAGATTTTGCACAGAGTCTCTCTGAACATACTGCCCCCAGAGGAAGAAGAAGAGAC  
CCATAAGATTGGCAGTCTGGCTGAGAACGCATTTCTCAGACCCCTGCAGGCAGTGCCAACCCTTT  
GGAACCCAGCCAGGATGAGAAGAGCATCCCCCTTGATCTGGGGTGCTGTGCTCCTGGTAGGTCT  
GCTGGTGGCAGCGGTGGTGTGTTTCTGTGATGGCCAAGAGGAAACAAGAATCCCTCCTCAG  
TGGTCCACCACGTCAGTGACTCTGGACCGGCTGTGAATTGCCTTTGGATGTACCACACATTA  
GGCTTGACTCACCACCTTCATTTGACAATACCACCTACACCAGCCTACCTCTTGATTCCCAT  
CAGGAAAACCTTCACTCCCAGCTCCATCCTCATTGCCCCCTCTACCTCCTAAGGTCCTGGTCT  
GCTCCAAGCCTGTGACATATGCCACAGTAATCTTCCCGGGAGGGAACAAGGTTGGAGGGACCT  
CGTGTGGGCCAGCCAGAATCCACCTAACAAATCAGACTCCATCCAGCTAAGCTGCTCATCACA  
CTTTAAACTCATGAGGACCATCCCTAGGGGTTCTGTGCATCCATCCAGCCAGCTCATGCCCTA  
GGATCCTTAGGATATCTGAGCAACCAGGGACTTTAAGATCTAATCCAATGTCTTAACCTTTACT  
AGGGAAAGTGACGCTCAGACATGACTGAGATGTCTTGGGGAAGACCTCCCTGCACCCAACTCC  
CCCACTGGTTCTTCTACCATTACACACTGGGCTAAATAAACCTAATAATGATGTGCAAAAAA  
AA

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**FIGURE 92**

MGLTLLLLLLGLLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRFLPEGCQPLV  
SSAVDRRAPAGRRTFLTLGGGLLQVEMVTLQEEDAGEYGCMDVGARGPQILHRVSLNILPPE  
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFVMAKRKQ  
ESLLSGPPRQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristoylation sites.**

amino acids 17-23, 172-178

**Amidation site.**

amino acids 73-79

[illegible]

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**FIGURE 94**

MEEGGGVRSILVPGGPVLLVLCGLLEASGGGRALPQLSDDIPFRVNWPGTEFSLPTTGVLVLYKE  
DNYVIMTTAHKEKYKCILPLVTSGDEEEEEKDYKGNPRELLEPLFKQSSCSYRIESYWTYEV  
HGKHIRQYHEEKEQKINIEHYLLGNMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMTPEY  
PVGMGNGTPCSLKQNRPRSTVMYICHPESEKHEILSVAEVTTCYEVVILTPLLCSHPKYRFR  
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVPPRRNKEGVGWKYEFCYGKHVHQYHEDK  
DSGKTSVVVGTVNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYGNQDIDITDKPRQVTV  
KLKCKESDSPHAVTVYMLEPHSCQYILGVESPVICKILDTADENGLLSLPN

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Glycosaminoglycan attachment site.**

amino acids 28-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 337-341

**N-myristoylation sites.**

amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,  
196-202

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

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**FIGURE 95**

TTCCGTTTCTGGGAGGAGTGAGGGGCAACGGGTCGGAGAAAAAGGAAAAAGAGGGCTCAGC  
GCCTCCCCCGCGGGCCGTGGACAGAGGGGCACAGTTTCGGCAGGCGGGTGAGGTCGCTGAGGG  
CCCGCCGGGAGATGTTTTCTTCTGTCGAGCAGGTCGAACCCAGGTTACAGTTCCTCTGAGTCA  
TCTCATCAATGCCTTCCATACACCAAAAAACACTTCTGTTCTCTCTAGTGAGTCTCAGTTTC  
TCAAAACCAGCATCGAGATGTAGTTCCTGAGCATGAGGCTCCAGCAGTGAGCCTTCACTTAA  
CTTAAGGGACCTTGGATTATCTGAACTAAAAATTGGACAGATTGATCAGCTGGTAGAAAAATCT  
ACTTCTGGATTTTGTAAAGGCAAAAAACATTCTTCCCATTTGGCATACATCCCATTGTCTCTGC  
ACAATCCTTCTTTGAAAAATAAATATGGTAACCTAGATATATTTAGTACATTACGTTCTCTTG  
CTTGTATCGACATCATTTCAAGAGCTCTTCAAGCATTTTGTTCAGATCTTCAGTACTGGCCAGT  
TTTCATACAGCTCTCGGGGTTTTAAAACTTTGAAATCAAGGACACGAGCTCTCCAGTCTACCTC  
CGAGAGATTAGCTGAAACACAGAATATAGCGCCATCATTCGTGAAGGGGTTTCTTTTGGGGGA  
CAGAGGATCAGATGTTGAGAGTTTGGACAACTCATGAAACCAAAAAATATACCTGAAGCTCA  
CCAAGATGCATTTAAAACTGGTTTTTGGGAGGTTTTCTGAAAGCTCAAGCACTCACACAAAA  
AACCAATGATPCCCTAAGGCGAACCCGCTCTGATTCTCTCGTCTGCTGCTATTTCGGCATTTA  
TGGACTTCTAAAAAACCCATTTTTATCTGTCCGCTTCCGGACACACAGGCGCTGATTCTGTCG  
AGTAGATCCTGTCTCAGATGCAAAATGTCACCTTTGAACATGTCAAGGGGTGGAGGAAGCTAA  
ACAAGAATTACAGGAAGTTGTTGAATCTTGA AAAATCCACAAAAATTTACTATTCTTGGAGG  
TAAACTTCCAAAAGGAATTTCTTTAGTTGGACCCCGAGGACTGGAAGACACTTCTTGCCCCG  
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTTATTATGCTTCTGGATCCGAATTTGATGAGAT  
GTTTGTGGGTGTGGGAGCCAGCGGTATCAGAAATCTTTTAGGGAAGCAAAGGCGAATGCTCC  
TTGTGTTATATTTATTTGATGAATTAGATTCTGTTGGTGGGAAGAAATTGAATCTCCAATGCA  
TCCATATTTCAAGGCAGACCATAAATCAACTCTTGTCTGAAATGGATGGTTTTAAACCCGAATGA  
AGGAGTTATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACGTCC  
TGGTCGTTTTGACATGCAAGTTACAGTTCGAAGGCCAGATGTAAAGGTCGAACAGAAATTTT  
GAAATGGTATCTCAATAAAATAAAGTTTGATCAATCCGTTGATCCAGAAATTATAGCTCGAGG  
TACTGTTGGCTTTTCCGGAGCAGAGTTGGAGAATCTTGTGAACCCAGGCTGCATTTAAAGCAGC  
TGTTGATGGA AAAAGAAATGGTTACCATGAAGGAGCTGGAGTTTTCCAAGACAAAATTTCTAAT  
GGGGCTGAAAGAGAAGATGTGGAAATTGATAACAAAAACAAACCTCACAGCATATCATGA  
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT  
CATGCCACGGGGGCCAACACTTGGACATGTGTCCCTGTTACCTGAGAAATGACAGATGGAATGA  
AAGTAGCGAGCTGCTGTCACAAATGGATGTAGTAGGGGAGGAGAGTGGCAGAGGAGCT  
TATATTTGGAACCGACCATATTACACAGGTGCTTCCAGTGATTTTGATAATGCCACTAAAAAT  
AGCAAAGCGGATGGTTACCAATTTGGAATGAGTGAAAAGCTTGGAGTTATGACCTACAGTGA  
TACAGGGAACCTAAGTCCAGAAACCAATCTGCCATCGAACAAGAAATAAGAAATCCTTCTAAG  
GGACTCATATGAACGAGCAAAACATATCTTGA AAACCTCATGCAAAGGAGCATAGAATCTCGC  
AGAAGCTTTTATGACCTATGAGACTTTGGATGCCAAAGAGATTTCAATTTGTTCTTGAGGGGAA  
AAAGTTGGAAGTGAGATGATAA ACTCTCTTGATATGGATGCTTCTGTGTTTTATTGCAAGAATA  
TAAGTAGCATTTGCAGTAGTCTACTTTTACACGCTTTCCCTCATTTCTGTATGTGGTGTAAAT  
GAAGGTGTGAAATGCTTTGTCAATCATTTGTACATTTATCCAGTTTGGGTTATTTCTCATT  
TGACACCTATTGCAAAATGCAATCCCATGGCAAAATATATTTTGA AAAATAAGAACTAGCAG  
GATTGAAAACAAAAA AAAAAA



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**FIGURE 96**

MFSLSSSTVQPQVTVPLSHLINAFHTPKNTSVSLSGVSVSQNHQHRDVPPEHEAPSSEPSLNLRD  
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFENKYGNLDIFSTLRSSCLYR  
HHSRALQSICSDLQYWPVFIQSRGFKTLKSRTTLLQSTSERLAETQNIAPSFVKGFLLRDRGS  
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDSLRRTLLILFVLLLFGIYGLL  
KNPFLSVRFRTTTGLDSAVDPVQMKNVTFEHVKGVEEAKQELQEVVEFLKNPQKFTILGGKLP  
KGILLVGPPGTGKTLARAVAGEADVPFYYASGSEFDEMFGVGASRIRNLFREAKANAPCVI  
FIDELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKNPNEGVIIGATNFPEALDNALIRPGRF  
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPETIIARGTVGFGAELENLVNQAALKAADV  
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAIAYYTKDAMPINKATIMPR  
GPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITGASSDFDNATKIAKR  
MVTKFGMSEKLGVMTYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL  
LTYETLDAKEIQIVLEGKKLEVR

**Important features of the protein:****Transmembrane domain:**

amino acids 238-259

**N-glycosylation sites.**amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,  
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

**Amidation site.**

amino acids 387-393, 709-713

**ATP/GTP-binding site motif A (P-loop).**

amino acids 322-330

**AAA-protein family proteins**

amino acids 315-336, 343-386, 405-451

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**FIGURE 97**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCTCTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCTCCAAA  
ACAAGTTTGTACATTTCCCTCGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTTCTCTCTGTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAAAATAACAGACCCCTGACCATTATACCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGCCTTTGGGGGAAGTACACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTGGCTATTTAATGTATTTATTTTTTACTTGGACATG  
AAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGATTTTTAT  
ACAGTAAAAAATTCCTGTAAATCTAGAAGAGTGGCTAGGGGGGTATTCACTTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATGAACCAATGAC  
TACTTAGGATGGGTTGTGGAATAAGTTTTGTGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATATTTGTGTATCTTCAGCCAGGAATCTTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 98**

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR  
ILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKISSLANSEFLT IKKDLRLC  
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

**Signal sequence:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 107-110, 140-143

**N-myristoylation site.**

amino acids 51-56

**Interleukin 10:**

amino acids 9-176



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**FIGURE 100**

MRLLPEWFLLLFPGPWLLRKAVSAQIPESGRPQYLGLRPAAAGAGAPGQQLPEPRSSDGLGVGR  
AWSWAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLLVTG  
KIVDHNVTFSVYFRHNSSSLGNLSVSI VPPSKRVEFGGVWLPGPVPHPLQSTLALLEGVLPGL  
GPPLCMAAAAAGPGLGSSLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD  
PSQVCFTENTQSQAAWLCAKPFKVICIEVSFLSFDYKLVQKVCPDYNFQSEHPYFG

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 273-288

**N-glycosylation sites.**

amino acids 72-76, 133-137, 143-147, 149-153

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 93-97

**N-myristoylation sites.**amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,  
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

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**FIGURE 101**

AATGCCCCATGCGCACCCCCACAGCTCGCGCTCCTGCAAGTGTTCTTTCTGGTGTCCCCGATG  
GCGTCCGGCCTCAGCCCTCTTCCTCCCCATCAGGGGAGTGGCCACGCTCTTTGGAGCTGCAGC  
GAGGGACGGATGGCGGAACCTCCAGTCCCCCTCAGAGGCGACTGCAACTCGCCCCGGCCGTGC  
CTGGACTCCCTACAGTGGTCCCTACTCTCGTGACTCCCTCGGCCCTGGGAATAGGACTGTGG  
ACCTCTTTCCAGTCTTACCAGTCTGTGTCTGTGACTTGACTCCTGGAGCCTGCATATAAAAT  
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTTCTCCTTCTGCCTTCCAG  
GCAGCGTAAGTCTTCAAGCTGGGTTTGTGTAGACAACCTCTGTTATCTTCAGGAGTAATTCCC  
CGTTTCCTTCAAGAGTTTTCATGGATTCTAATGGAATCAGGCAGTTTTTGTGTCCATGTGAACA  
ACTCAAACCTAAACTATTTCCAGAAGCTTCAAAGGTCAATGCAACCAACTTCCAGGCCCTGG  
CTGCAGAGTTTTGGAGGCGAATCATTCACTTCAACATTCCAAACTCAATCACCACCATCTTTTT  
ACAGGGCTGGGGACCCCATCTTACTTACTTCCCCAAGTGGTCTGTAATAAGCTTGCTGAGAC  
AACTTGCAGGAGTTGGAGCTGGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTTCTAGAGA  
GTAAAGTACAACCTTGCACTCGTTTTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTGAG  
CCCTCAATGCTGCCTCTTACTATAACTTCACAGTCTTAAAGGTTCCAAGAAGCATGACTGATC  
CACAGAATATGGAGTTCCAGGTTTCTGTAATACTTACCTCACAGGCTAATGCTCCTCTGTTGG  
CTGGAAACACTTGTGAGAATGTAGTTTTCTCAGGTCACCTATGAGATAGAGACCAATGGGACTT  
TTGGAATCCAGAAACTTTCTGTGAGTTTGGGACAAACCAACCTGACTGTTGAGCCAGGCGCTT  
CCTTACAGCAACACTTCATCCTTCGCTTCAGGGCTTTTCAACAGAGCACAGCTGCTTCTCTCA  
CCAGTCTAGAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTTGGCTCTGACTGATG  
ATATAAGTTACTCAATGACCTCTTACAGAGCCAGGGTAATGGAAGTTGCTCTGTGTTAAAGAC  
ATGAAGTGCAGTTTGGAGTGAATGCAATATCTGGATGCAAGCTCAGGTTGAAGAAGGCAGACT  
GCAGCCACTTGCAGCAGGAGATTTATCAGACTCTTCATGGAAGGCCAGACCAGAGTATGTTG  
CCATCTTTGGTAATGCTGACCCAGCCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGCAT  
GCAGCATTTAGCTATAAACTGTACTTCTGCTGTCTCATACCAGTTTCCCTGGAGATCCAGG  
TATTGTGGGCATATGTAGGTCTCCTGTCCAACCCGCAAGCTCATGTATCAGGAGTTCGATTCC  
TATACCAGTGCCAGTCTATACAGGATTCTCAGCAAGTTACAGAAGTATCTTTGACAACCTCTTG  
TGAACCTTTGTGGACATTACCAGAAAGCCACAGCCTCCAAGGGGCCAACCCAAAATGGACTGGA  
AATGGCCATTGCACTTCTTTCCCTTCAAAGTGGCATTGAGCAGAGGAGTATTCTCTCAAAAAT  
GCTCAGTCTCTCCCATCCTTATCCTGTGCTCTTACTACTTGGAGTTCTCAACCTAGAGACTA  
TGTGAAGAAAAAGAAAATAATCAGATTTCAAGTTTTCCCTATGAGAACTCTGAGGCAGCCACTT  
ATCTTGGCTAAATAGAACCTCACCTGCTCATGACCAGAGAGCATTTAGGATAATAGATGACCT  
AACTGAAGGAATCCTTGTATATGAAAGGAGTTATTTTAGAAAAGCAATAAAAAATATTTTATTC  
ATCNTAAAAA

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**FIGURE 102**

MRTPLQALLQVFFLVFPDGVPRQPSSSPSGAVPTSLELQRGTDGGTLQSPSEATATRPVAVPGL  
PTVVPTLVTPSAPGNRTVDLFPVLPICVCDLTPGACDINCCCDRCYLLHPRTVFSFCLPGSV  
RSSSWVCVDNSVIFRSNSPFPSRVFMDSENGIRQFCVHVNSNLNYFQKLQKVNATNFQALAAE  
EGGESFTSTFTQSPSPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS  
TTCTRFFKNLASSCTLDSALNAASYNFETVLKVPMSMTDPQNMEFQVPEVILTSQANAPLLAGN  
TCQNVVSQVTYELETNGTFGIQKVSVSLGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP  
RSGNPGYIVGKPLLALTDISYSMTLLQSQNGSGCSVKRHEVQFGVNAISGCKLRLKKADCSH  
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW  
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTTLVNFVDITQKPQPPRGQPKMDWKWP  
EDFFPFKVAFSRGVFSQKCSVSPILILCLLLLGVNLLETM

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites.**amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,  
410-414, 487-491**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 420-431

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**FIGURE 103**

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGAGGCCATGTGGGAT  
TAAGAAGTGATAGGAGAGCTTGTCTGTCTGTCTCTCCACTGTGTGAGGATACAACAGGA  
AGACAGCCATCTGGTGAGGAAGAGAGGGCCCTCGCCAGATACCGGACCTGCTGACACCTTGAT  
CTTGACTTCCCATCTTCCAGGAAGGCTGACCTCAGTTGTTCCAGGGTAAAGAATTTGGGCA  
GTGCCCCACCCACGCTGTTGGATAACATTTCTTCACCATACCACTGAGGGTGAATGTGTACA  
CGCCAGCTTCTGCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG  
TGCGCCTTCTTTTGTCTGCTGTTGCTACTAATAGCCTTGGAGATCATGGTTGGTGGTCACT  
CTCTTTGCTTCAACTTCACTATAAAATCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGC  
AGGTCTTCTTGAATAAAAATCTTTTCTTCACTACAACAGTGACAACAACATGGTCAAACCTC  
TGGGCCCTCTGGGAAGAAGGTATATGCCACCAGCACTTGGGGAGAATTGACCCAAACGCTGG  
GAGAAGTGGGGCAGACCTCAGGATGCTCCTTTGTGACATCAAAACCCAGATAAAGACCACTG  
ATCCTTCCACTCTGCAAGTCGAGATGTTTTGTCAACGTGAAGCAGAACGGTGCATCTGGTGCAT  
CCTGGCAGTTTCGCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGA  
CAGTAATTAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA  
AGTATTTTCAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGAATCTTAGGGCACT  
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACCTAGAGGTGATACCACGGCGGCGCAG  
AGTTGTTACCTGTGGTCTCGATCGCTGACAGCCTTGGCTCCCCTGCTGTGTGTTCCCTGA  
GTCAAGTGGAGGCGGAGCCTGCAATGAGCGGAGATCGCGCCTCTGCATTCCAGCTCTTGGCAAC  
AGAGCAAGACTCCGCTCTCAAAAAAAAAAATTTTTTTCAGTACATATTTTTTAAAGATAGG  
GCTGGGCACAGCAGCTCACATCTATAATCCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC  
TTGAGCCAGGAATCTGAAGCTGCAGTGAGCCTTTGCTCGTGAGATTGTGGACCTATGATCCT  
ACCACCAGCCACCTGGTTCTAACACCCCTCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG  
AGGGAGAAAAGAGAGATAAGCAAGAACAGAGAGGAAAAATGGAATAAAGAGGAATTTGGGG  
GAATTAACAGAGGGGAGGGCATGGATCCCCGGGAGTTAGAAGAGTAGCAGCTTGTGGATTAC  
TACGCAGTGGAGGAAGAAGATTGTTGGAATATTTGAGAGGTAGTATAATCATTTGTGAGG  
CAGTTTTCTGCATTACCATTTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTCACA  
TTACACTGAAATCTTCCTAATACATCATTTGCATTGGAATAAAGTACGGTTTTCAAACAAC  
CTGATATAGCAGAACTGACTGTATAAATATGTGAGCACAGTGCAAGTAATCTTTGTTTGT  
TGTTTGTTTTTTGGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCATCC  
CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCTGCTCAGCCTCCTGAGTAG  
CTGGGATTACAGGCATGAGCCACCACGCGGCTAATTTTTGTATTTTAGTAGAGACGGGT  
TTCACCTGTGGCCAGGCTGGTCTCGAACTACGGACCTCAGGTGATCTGCCCCCTCAGCCT  
CTCAAAGTGTGGGATTATAGCATGAGCCACTGAGCCAGACACAAGTAGTTCTTTCTGATAA  
ACACTTTAACACTGAATGCA



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**FIGURE 104**

MRRISLTSSPVRLLLLFLLLLLIALEIMVGGHSLCFNFTIKSLSRPGQPWCEAQVFLNKNLFLQ  
YNSDNNMVKPLGLLGKKVYATSTWGELTQTLGEVGRDLRMLLCDIKPQIKTSDPSTLQVEMFC  
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGC  
DHWLREFLGHWEAMPEPTGRRST

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 11-30(possible type II protein)

**N-glycosylation site.**

amino acids 36-39, 154-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-5, 182-185, 209-212

**Casein kinase II phosphorylation site.**

amino acids 86-89, 93-96, 142-145, 185-188

**N-myristoylation site.**

amino acids 46-51

**Amidation site.**

amino acids 77-80, 207-210

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**FIGURE 105**

TTTTCCGAGTGACCTTCTTGTATGCTGGCTGTTTCTCTCACCGTTCCCCTGCTTGGAGCCATGA  
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTTCAAAGAACCCCCGCTCTTGCTTG  
GTGTTCTGCATCCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTTGAAAATCAACTTGTTG  
GACCGGAGTCCATAGACATATTGGGGATGTGATGTTTACTGGGACAGCAGATGGCCGGGTCG  
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCCGGTTTGGTTGCGGGCCCTTGCAAAACCC  
GAGATGATGAGCCTGTGTGTGGGAGACCCTGGGTATCCGTCGAGGGCCCAATGGGACTCTCT  
TTGTGGCCGATGCATACAAGGGACTATTTGAAGTAAATCCCTGGAACGTGAAGTGAAGTGC  
TGCTGTCTCCGAGACACCCATTGAGGGGAAGAACATGTCTTTTGTGAATGATCTTACAGTCA  
CTCAGGATGGGAGGAAGATTATTTACCGATTCTAGCAGCAAAATGGCAAAGACGAGACTACC  
TGCTTCTGGTGATGGAGGGCACAGATGACGGGCGCCTGCTGGAGTATGATACTGTGACCAGGG  
AAGTAAAGTTTTATTGGACCAGCTGCGGTTCGCCAATGGAGTCCAGCTGTCTCCTGCAAGAG  
ACTTGTCTCTGGTGGCAGAAACAACCATGGCCAGGATACGAAGAGTCTACGTTTCTGGCCTGA  
TGAAGGGCGGGGCTGATCTGTTTGTGGAGAACATGCCTGGATTTCAGACAACATCCGGCCCA  
GCAGCTCTGGGGGGTACTGGGTGGGCATGTGACCATCCGCCCTAACCTGGGTTTTCCATGC  
TGGATTTCTTATCTGAGAGACCCCTGGATTAAAAGGATGATTTTTAAGCTCTTTAGTCAAGAGA  
CGGTGATGAAGTTTGTGCCGCGGTACAGCCTCGTCTCTAGAACTCAGCGACAGCGGTGCCTTCC  
GGAGAAGCCTGCATGATCCCGATGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG  
ATGGGCACCTGTACCTGGGCTCTTTAGGTCCCCCTTCCTCTGCAGACTCAGCCTCCAGGCTG  
TTTAGCCCTCCAGATAGCTGCCCTGCCACGAGGCCAGGAGTCTTCACTCAGGCACCAG  
GCCTGGTCCAGGAGGAGCTGTGGACACAGTCTGGTTCAAGTGTCCACATGCACCTGTTAGTC  
CCTGAGAGGTGTTGGGAATGGCTGCTTCACTTCCCTCGAGGATGCCCGGGCCCCAOCCTGGGCTTG  
TCTTTCTGTTTATAGAGGAAGTGTAACATATCTGCCATGAGGAACATAAATTCTATGTAAGCCA  
TTTTCTCTTAAACAAAAACAAACTTTCTAAGTACAATCATTTCTCTAGGATTTGGGAAGCTCCT  
TGCACTTGGAACAGGGCTCAGGTGGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG  
CGGCCCTGTCTGCGGCCTCAAAGTTTCTTTTACTATATATAACGTGCGGTGCATACCTTTCT  
TCGTTGTGGTGGGGATGGAAGAGCAGAGGGAGCATGGCCCAGGGGTGTTGAGGCCAGCGGTGA  
GAGCCGTGTTAGCCAAGACATGGAACGTGTTCTCAAGGGTTATGTGGGGCGTGGGCTCTCCA  
TAGTGTGTATGAAAAGCTTGTGACTCTAGCGGCTCAGAGAGGACTTTGCTGGGTTTCTTTCT  
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTCGGGACCTACTGCAG  
GGGTCCGTTTAGTAACGTCTTGTCTGTGATCTTTGTTCTTGACCTCTAGACCCCAAGATGTGA  
ACAGTGCACGTGTTAATGTCATCTTTGCTCATGTGTTATAAGCCCCAAGTTGCTGTATATTT  
CACAAGTATGTCTACACACTGG

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**FIGURE 106**

MLAVSLTVPLL GAMMLES PIDPQPLSFKEP LLLGLV LHPNTKLRQAERLFENQLVGPESIAH  
IGDVMFTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYK  
GLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG  
TDDGRLLLEYDTVTREVKVLDDQLRFPNGVQLSPAEDFVLVAETTMARIRRVYVSGLMKGGADL  
EVENMPGFPDNI RPS SGGYWVG MSTIRPNPGFSMLDFL SERPWIKRMIFK LFSQETVMKFVP  
RYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHL YLGSFRSPFLCRLSLQAV

**Important features of the protein:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 1-21 (possible type II)

**N-glycosylation sites.**

amino acids 116-119, 152-155

**Casein kinase II phosphorylation sites.**

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

**N-myristoylation sites.**

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

**Amidation site.**

amino acids 164-167

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**FIGURE 107**

AACGAAGCGTGC GCGCTTTGGTAACCGGCTAGAAATCCGCGACGCGCGCCTGCCTCCTCTCCC  
CAGGCGCTGAGCTGCCCCCTCCCACTGCCTTTCTCTTCTCCCGGAGTCAGAAAGCTTCGGGAGGG  
CCCAGAGAGGGCGGTGGGGTGGGCGACCCCTACGCCAGCTCCGGGGCGGAGAAAGCCCCACCTCT  
CCCCGCGCCCCAGGAAACGCCGCGCTTCGGCGCTGCGCAGAGCCATGGGAATTCCTCTGGCTGG  
AGACGCGCTGGGCGCGGCCCTTTTACCTGGCGTTCGTGTTCTGCCTGGCCCTGGGGCTGCTGC  
AGGCCATTAAAGCTGTACCTGCGGAGGACAGCGGCTGCTGCGGGACCTGCGGCCCTTCCCAGCGC  
CCCCACCCACTGGTTCTTGGGCACCAGAAATTTATTCAGGATGATAACATGGAGAAGCTTG  
AGGAAATTATTGAAAAATACCCCTCGTGCCTTCCCTTTCTGGATTGGGCCCTTTTCAGGCATTTT  
TCTGTATCTATGACCAGACTATGCAAAGACACTTCTGAGCAGAAACAGATCCCAAGTCCCAGT  
ACCTGCAGAAATTCACCTCCACTTCTTGGAAAAGGACTAGCGGCTCTAGACGGACCCAAGT  
GGTTCAGCATCGTCGCTACTAACTCCTGGATTCCATTTTAACATCCTGAAAGCATACATTG  
AGGTGATGGCTCATTTCTGTGAAAATGATGCTGGATAAGTGGGAGAAGATTTGCAGCACTCAGG  
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTCTGGATATAATCATGAAATGCG  
CTTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAGCCATAT  
TTGAACTCAGCAAAATCATATTTACCCGCTTGTACAGTTTGTGTATCACAGTGACATAATTT  
TCAAACCTCAGCCCTCAGGGCTACCGCTTCCAGAAGTTAAGCCGATGTTGAATCAGTACACAG  
ATACAATAATCCAGGAAAGAAAGAAATCCCTCCAGGCTGGGGTAAAGCAGGATAACACTCCGA  
AGAGGAAGTACCAGGATTTTCTGGATATTGTCCTTTCTGCCAAGGATGAAAGTGGTAGCAGCT  
TCTCAGATATTGATGTACACTCTGAAGTGAGCACATTCCTGTTGGCAGGACATGACACCTTGG  
CAGCAAGCATCTCCTGGATCCTTTACTGCCTGGCTCTGAACCTGAGCATCAAGAGAGATGCC  
GGGAGGAGGTACAGGGGCATCCTGGGGATGGGTCTTCTATCACTTGGGACCAGCTGGGTGAGA  
TGTGCTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTCGAGTCCCGTCCATTT  
CCAGAGATCTCAGCAAGCCACTTACCTTCCCAGATGGATGCACATTGCCTGCAGGGATCACCG  
TGTTCTTAGTATTTGGGGTCTTCAACCAACCCCTGCTGTCTGGAAAAACCCAAAGGTCTTTG  
ACCCCTTGAGGTTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCCTACTTACCATTCT  
CAGCTGGATCAAGGAACTGCATTGGGCAGGAGTTTGCCATGATTGAGTTAAAGGTAACCATTG  
CCTTGATTCTGCTCCACTTCAGAGTGACTCCAGACCCACCCAGGCTCTTACTTTCCCCAAC  
ATTTTATCCTCAAGCCCCAAGAATGGGATGTATTTGCACCTGAAGAAACTCTCTGAATGTAGAG  
TCTCAGGGTACAATGATTAAACGTACTTTGTTTTTCGAAGTTAAATTTACAGCTAATGATCCA  
AGCAGATAGAAAGGGATCAATGTATGGTGGGAGGATGGAGGTTGGTGGGATAGGGGTCTCTG  
TGAAGAGATCCAAAAATCATTCTAGGTACACAGTGTGTCACTAGATCTGTTTCTATATAAAT  
TTGGGAGATTTTCAGATCTTTTCTGTTAAACTTTCCTACTATTAATGCTGTATACACCAATA  
GACTTTCATATATTTCTGTTGTTTTTAAATAGTTTTCAGAATTATGCAAGTAATAAGTGCA  
TGTATGCTACGTGTCAGAAAATCCCAACACTAGAAAATCATGTAGAAATAAAAAATTTTAAATCT  
CACTTCACCTTAGCCGACATTCCATGCCCTGACCAATCCTACTGCTTTTCTTAAAAACAGAATA  
ATTTGGTGTGATCTTTTCAGACTTTTTCCTATACATTTTATATGTAGAAATGTAGCAATGTA  
TTTGTATAGATGTGATCATTCCCTATATTGTTATGATTTTTTTCACTTAATAAAAAATTCACCT  
TATTCCTTAAAA

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**FIGURE 108**

MEFSWLETRWARPFYLAFFVCLALGLLQAIKLYLRRQRLRLDRPFPAPPTHWFLGHQKFIQD  
DNMEKLEEIIIEKYPRAFPFWIGPQAFFCIYDPDYAKTLLSRTDPKSQYLQKFSPLLKGKGLA  
ALDGPKEWFQHRRLTTPGFHFHNLKAYIEVMAHSVKMMLDKWEKICSTQDTSVEVYEHINSMSL  
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDIIFKLSPQGYRFQKLSR  
VLNQYTDITIQRKKSLQAGVKQDNTPKRKYQDFLDIVLSAKDESGSSFSDDIVHSEVSTFLL  
AGHDTLAASISWILYCLALNPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCRLI  
PAVPSISRDLSEKPLTFPDGCTLPAGITVVLISWGLHHNPAVWKNPKVFDPLRFSQENSDDQRHP  
YAYLPFSAGSRNCIGQEFAMIELKVTIALILLHFRVTPDPTRPLTFPNHFIKPKNGMYLHLK  
KLSEC

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 310-330, 397-413, 459-473

**N-glycosylation site.**

amino acids 206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 265-269, 504-520

**N-myristoylation sites.**

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 447-457

**Cytochrome P450 cysteine heme-iron ligand proteins.**

amino acids 444-475

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**FIGURE 109**

GGCGTTCGGGGCTCAACTTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC  
AGCAATTTTGCTTCTTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCTCGGATTCTGAGAT  
CCAGACCAGCTCCTCCAGACCTCTCCAGAAGAAGCCATGGGAACCCCTCGTATCCAGCATTT  
GCTGATCCTCCTGGTCCTAGGAGCCTCCCTCCTGACCTCGGGCCTAGAGCTGTATTGTCAAAA  
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTTAACTGGACCACAGAGGAAGT  
GGAGACTTGTGACAAAGGGGCACTTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA  
GACAGCCATTTTGGCCACGAAGGGCTGCATCCCGGAAGGGGAGGAGGCCATAACAATTGTCCA  
GCACTCTTCACCTCCCGGCCTGATCGTGACCTCCTACAGTAACTACTGTGAGGATTCCTTCTG  
TAATGACAAAGACAGCCTGTCTCAGTTTGGGAGTTCAGTGAGACCACAGCTTCCACTGTGTC  
AACAAACCTCCATTGTCCAACCTGTGTGGCTTTGGGGACCTGTTTCAGTGCTCCTTCTCTCC  
CTGTCCCAATGGTACAACTCGATGCTATCAAGGAAAACCTTGAGATCACTGGAGGTGGCATTGA  
GTCGTCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGCTGTGGAATCTT  
AGCAGTAGGACCCATGTTTGTGAGGGAAGCGTGCCACATCAGCTGCTCACTCAACCTCGAAA  
GACTGAAAATGGGGCCACCTGTCTTCCCATTCTGTTTGGGGGTTACAGCTACTGCTGCCATT  
GCTGCTGCCATCATTTATTCACTTTTCCTAAGGAAGGCACTTCTGGGCCTGGGTCTGAGGACAT  
CTTTTTTGACTGGGAGCCTTCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT  
GAGGGAGAATACAGAGATACTATGAACGTATTTGACATTTTAAATACAATTTCTGCTATAATT  
TTTGTATGCAGTAGGCGTTACTAATAAACATTTCTGCTGTGA

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**FIGURE 110**

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVETCDKGALCQET  
ILIIKAGTETAILATKGCIP EGEEAITIVQHSSPPGLIVTSYSNYCEDSFCDKDSLSQFWEF  
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQKGLEITGGGIESSVEVKGCTAMI  
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVWGLQLLLPLLLPSFIHFS

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 184-201

**N-glycosylation sites.**

amino acids 45-49, 159-163

**N-myristoylation sites.**amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,  
175-181

FIGURE 111

CGAAGAGGGGACAGGAACTCTGAGCAAAAGGGGGTGGGCTTCAGGGCGACCCCTTAGCCCAATTCTGCCCTTCACAT  
ACCGAAAGAGATAAACCGGAGACGGGAGAGGCTGTGGCCAGCCAGTTACTTAGAGAGGCCACAGAGGAGAGAGCTCGGG  
TGAGTTCGCCATGGGGACTCCAGGGGCGGCAGCAGCGCGCTCCCGAGCTTGCTTCTTAATCTGTGTGAGTGT  
CTCCGGATCGAGGCTGTGCCCTCTGAAGGAGGAGAGATTTAGCCAGAGCTGGAAGTGAAGCCCGCAGCTGTGCC  
CTGTAGGCCCCCTGGCTGAATCGTCTCATGGGCGCCCTCTGTAGAGGGGGCCGAGAGATGGGCTACCTCGCAGGATCT  
TAGTCGGACCCACCGACTGAGCCACCCCTCGGGCGGCGAGACTTCGCAATGCCCTCCCTGCCACGGGCCACTGAG  
CCGGGACAGAGGGCTCTGCAACACAGCGCTCACCCTCAACCGGCTCAGGGGGGACGGCCCACTCGGCACAGCACT  
CTGACCCTCCGCCAGGAAACACAGCCGCCACCTGACACCGGCTCGTCTCCCGAGGCTCCCTCTTGGGCTCTG  
GGAGGAGAGGAGGAGACGACGACCCACATCATCACCGACCACTGTACCACATACGGTGAACCCAGCCAGCTCTG  
TGTAATAACAACATCTCCGAGGGCGAAGGATATGTGAAGTCTCCAGATCTGGGAGCCCTCGACGCCACCTCTG  
GGGCTCTCTGGACTGCACTTACAGCATCACTGTCACTGGCTGCGTACCGGATAGAGATCAGGTGCAGACGCTGAAC  
CTGTACAGGAGAGGAGAGCTCTGGTGTGGCTGTGGGGGATCCCGAGGCTGBCGCCGCCCACTCTGGCCAC  
TCTACATCTGCTTGACAGGACCAAGTCTCTGGAGCCCAACCAACCGGCTCTCTGCACTTCAGAGCCACGG  
GTCCCAAGGGGCGGGCTGGCTTCAGATCCATCTATGAGGCCCTACTCTCTGAGCTGTGGCTCCCTCCCGGCGCGCC  
CTAGGGAGCTGTGAGTGTGACGAGCTGACCTTCGGGGGACCTGCCACCTTTCACTGTGATTGGGCTACAGGCT  
CAGGAGAGGAGACCTCTATCTGCTCCATATGGCAACCGCCGATCTCGGAAGGCTGAACCCCAAGCTGCATGGCA  
TCTGTGGTGGACCTATCCAAATGCGACCTGGGCGGCTCTGTGTCCGAGAGCTGTGGGGAGCCCTTAGGGGCC  
AACCTCACCTGCCGTTGGGTCATTGAAGCAGCTGAGGGGCGCCGGCTGCACCTGCATTTGAAGAGGCTCTCGCT  
GTAGGAGCAATGACCGGCTATGTTGGCGCTCAGGGGAGCCCTCATTCGCCGTGATCTATGATTGGGACATG  
GACATGTGCCCGAGGGGGTCTCATGATGACCGGAGCTCTCTACGTGAGAGCTGCTGTACAGACACCTGTG  
ATTCCTCTGCTGTGTAAAGCTCTGATTTGAGGCTCTTAGGAGAGATCGCTGTCTGCCCCCTCTGTGCACTAG  
AATGTCTACTACCGAGCCCTGAGTATGCGCCAGGGGACATGGCAACCTTTCTGTGCTCCGAGATATGCTCT  
GAGCGGCTGGGCGCCCAATGSCATCGAATGTGTGGATCCACAGAACCCCACTGGAAAGCAGCACGCGCCGCT  
TGCAGAACCATGTGTGGAGGGAGCTGTGCGAAGCACTGGCGTGTCTCTCTCCGACTGGCCCGACAGCAT  
AGCCCGGCGCAAGATTCGCTGTGGGGCGTGACCTCTCAGGAGAGAACAGGCATCTGTGCTCCAAATGTAGATATT  
AATGTGTCGGGAGAGGAGATGCTGACGCTGTCTGACGGGAGCGTGGCAGGCCGAGTCTGGCCCACTGTGGG  
GGACCTCAGCGCGCGCGCGCTCTCTCTCTGTGGGCGGACCTTCACATTCGATTTACGGAACCGCGCCGCT  
CCAAATCCAGGAGCTGTGGGCGAGGCTCTGTTATGCACTTCAAGAGGATCCGAGGAGACGACGCTGCCGAGCTC  
CACAATCCGAGATGGGGCTGTGAGAACGSCATCCACGGGACCTGTATCGGGGACAGGCTGCTCACTACAGTGC  
GAGCTCGCAATCAGAGCTGTAGGCTCGCATCTTCTCATTCGCAATGGGACCTGTCTGTGAGCGCGCGCGCGCC  
GGCTCGGAAAGATCTATGATTTGTGTGACCTGCGAGATTTGCCAAGGGGACCGCAGCCGCTCGGACGCGCG  
TTCGCCGTTGGCTCCCACTTCGATACCGCTGCTGTGAGGAGTACAGCTCGAGGGGCGAGCCATGCTCACTG  
TACAGCGGGGACAGGACCACTCAAGTGGAGCATAGGTTCCCAATTTGGCCTTGAAGTACAGCGCGTGCTCT  
AATCCGGGGGTTCCCGAATAGGCTACCAAGGCTGTATCAAGACAGCACTTACAGGCGGGCGAGCTCTGTGCGCTCT  
TCTGCTATGAGGCTTTGAGCTTGTGCGGAGGTTACCATCACTGTGTGCCCGGAGCTCCGATCCGATGGGAC  
AGCCAGCCCCCACTCTGCCAATGACCCAGACCAAGATCCATCAGGCACTGGGAAGGGGAGCACTGTGCCCTG  
GGCTCTGCTGTGCTCTCAGGCTTGGTCAATGTCTCGGCACTGGGCTTTACATCTACTACCAAGCTTCAGGGA  
AGATCCCTTTTTCGGCTCTCTCGGGCTCCCACTCTACAGGCCCCATCAGCGTGGAGTCGCACTTCAGCAACCGCTG  
TATGAAGCTGGGATACCGGGGATATGAAGATTTCCATCTGAACCCCAAGCTACAGCTCAGGACCGACGAGCG  
CCCTCCCTCTCTATTTCGGGACAGGAGGAATACGGGACCGGCTCTGCTCTGCTGCTGCCCTCTCTCTCGGCTG  
TGTAATATGCTCCCTATCCACAGGGGGGCTTGTATGGGCTGGAGATPCTCAGATAAATAAACCAAGCATCTGTG  
CCGCCAAAAA



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**FIGURE 112**

MGT PRAQHPPPPQLLLFILLSCFWIQGLPLKEEILPEPGSETPTVASEALAE LLHGALLRRG  
 PEMGYLP GSDPDTLATPPAGQTLAVPSLPRATEPGTGPLTTAVTPNGVRGAGPTAPELLTTP  
 PGTTAPPPPPSPASPGPLPPEGEGEEETTTTIIITTTT VTTTSPVLCNNNISEGEGYVESPD  
 GSPVSR TLGLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELLVLAGGSGPLAPRLLANSSMLG  
 EGQVLRSP TNRLLLHFQSPRVPRGGGFRIHYQAYLLSCGFPPRPAHG DVSVTDLHPGGTATFH  
 CDSGYQLQGEETL ICLNGTRPSWNGETPSCMASCGGTIHNATLGRIVSPEPGGAVGPNLTCRW  
 VIEAAEGRRLLHLHFERVSLDEDNDRMLMVRSGGSPLSPVIYDSMDDDVPERGLISDAQSLYVEL  
 LSETPANPLLLSLRFEAFEEDRCFAPFLAHGNVTTT DPEYRPGALATFSCLPGYALEPPGPPN  
 AIECVDPTEPHWNDETPACKAMCGGELSEPA GVVLPSPDWQSPSYSPGQDCVWGVHVQEEKRILL  
 QVEILNVREGDMLTLFDGDGSPARVLAQLRGQPQRRRLSSGPD LTLQFQAPP GPPNPGLGQG  
 FVLHFKEVPRNDTCPELPPPEWGWRTASHGDLIRGTVLTYQCEPGYELLGSDILTCQWDLWS  
 AAPACQKIMTCADPGEIANGHRTASDAGFPV GSHVQYRCPLPGYSLEGAAMLTCYSRDTGTPK  
 WSDRVPKALKYEPCLNPGVPENGYQTYLKH YQAGESLRFFCYEGFELIGEVTITCPVGHPS  
 QWTSQPLCKVTQTTPDSRQLEGGNLALAILLPLGLVIVL GSGVYIYYTKLQKSLFGFSGSH  
 SYSPI TVESDFS NPLYEAGDTREYEVSI

**Important features of the protein:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 842-864

**N-glycosylation sites.**

amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,  
473-477, 517-521, 641-645

**Tyrosine kinase phosphorylation site.**

amino acids 61-69

**N-myristoylation sites.**

amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,  
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,  
626-632, 665-671, 775-781, 842-848

**Amidation site.**

amino acids 384-388

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**CUB domain proteins profile.**

amino acids 202-218, 376-392, 553-569

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**FIGURE 113**

GCGCGGGGCGGAGCTGCCTGCCGGTCCGCGCGCGCGCTCCGCACTCTCGGCCCTCGGGCGGTGATGGGACGG  
 GCGCGCGCGGAGCAGGAGGCGGCGCCCGTCCGGGGTGCTCGGGCGCGCGGGAGCCACTGTGGGGCTCGGGCATG  
 GCGGGCGCGAGGACCTTGAGCTCTCTCAGGGGAGCGGGAGGCACTGCTGGCGGGCGATGGGAGCGGATGGGG  
 CGGTGCCGCGCGCGCGGACCGCTGAGCGCGGAGCCACGCGCGCGCTACTCAGCCCTCGCGAAAGCGCGGGGA  
 GCTCGGGAAAGC**ATG**CGCCCTGGAGCGGCTCTCTCGGTCTCAAAGTGTCTTAAACAGTACTTGGTAGTGGAAAG  
 GATTGCCGTGGCCCAAAAAACCAAGATGGACAAATATTGGGAATCAAGCATATTCTCGCAACCCAGTGTGGCAT  
 TGGGTTTCGAACAGCAATGGAGGTCATTTTGCTTCGCCAAATATCTGACTCATATCCACCAAAACAAGAGTG  
 TATCTACATTTTGGAGGCTGCTCCACGTCAAAGAATAGAGTTGACCTTTGATGARCATTTATATATAGAACCATC  
 ATTTGAGTGTCCGTTTGATCACTTGGAAAGTTCGAGATGGGCCATTTGGTTTCTCTCCTCTTATAGATCGTTACTG  
 TGGCGTGAAAGCCCTCCATTAATTAGATCAACAGGGAGATTCACTGGGATTAAAGTTTAGTTCTGATGAAGAGCT  
 TGAAGGACTGGGATTTCCGAGCAAAATATTCATTATTCCAGATCCAGACTTACTTACCTAGGAGGTATTTTAAA  
 TCCCATTTCCAGATTGTCAAGTTCGAGCTCTCGGGAGCTGATGGAATAGTGCCTCTAGTCAGGTAGAACAAAGGA  
 GAAACAAACCAAGCCAGCCAGCGTTGATTGCATCTGGACCATTAAGCCACTCCAAAGGCTAAGATTATTTGAG  
 GTTCTAGATTATCAAAATGGAGCACTCAAATGAATGACGAGAAACTTCGTTGCAGTCTATGATGGAAGCAGTTT  
 TATTGAAACCTGAAGGCCAAGTTTTCAGCAGCTGTGGCCAAATGATGTAATGCTTAAACAGGAATTTGGAGTGT  
 TCGAATGTGGGCGAGATGAAGGTAGTCGGCTTACGAGGTTTCGAATGCTCTTACTTCCCTTTGTGGAGCCTCCCTG  
 CACAAGCAGCACTTTCTTTTGCCATAGCAACATGTCGATCAATAATTTCTTAGTCTGTAATGGTGTCCAAATATG  
 TGCATACCCCTGGGATGAAATCATTTGAAAGAAAGAAAGCAGGAGTATTTGAACAAATCACTAAGACTCA  
 TGGAACAAATTATTTGGCATCTTCAGGGATTGTCTTGGTCCCTCTCATATTTTCTTTTAGTACAGGTGAAACA  
 GCCTCGAAAAAAGGTGATGGCTTGCAAAACCCGCTTTAATAAAACCGGGTTCGAAGAGTGTGTGATCCTCCTCA  
 TTATGAAGCTGTCTTCACTAAGGGAACAAGAGATTTCTGCAGACCTGGCAGACTGTGCGGAAGAAATTGGACAACTA  
 CCAGAAAGTGCGGCGCTCTCCACCGGCTCCCGCTGCATCCACGACCCCACTGTGGGTGCGAGGCTCCAGCGCT  
 CAAACAAAGCAGGACCAACCTCAGTTCCTATGGAACCTCCTTTCCGAAATGACTTTGCAACACCAAGCCCAATGAA  
 AACATTTAATAGCACTTCAAGAAAGTAGTTACACTTTCAAACAGGACATGAGTGCCCTGAGCAGGCCCTGGA  
 AGACCGAGTATGGAGGAGATTCCCTGTGAATTTATGTGAGGGGCGAGAAGATCTGCACAGCATCCATATC  
 CATTGACTTCA**TAAT**CTCTCTCTTAATGTTGATGTGAATTTCTTAGGGTGTGATGTCAGTACAGCCCTCCAGGGCAGCAT  
 ACTGTTTCCAGCAGCCAAACCTTTTCTCCCATCACAACACTCAGAAGACCTTGATTTACCGTTAACTTTGATGG  
 TGATGTTTTTATCTCTCAGGCACTGTATATATGTTAAACCAATCAAGGAATTTACTCTATTACAGTGAACAAAT  
 AATCATCTCTATTGCTTGGTGTCAATTTATAGGAAGCACTGCCAGTTAAAGAGCATAGAAGAGGTGGTTGGATGG  
 AGCCAGGCTCAGGCTGCCCTTCGTTTTAGCAACAAGAAGACTGCTCTTGACTGATACAGCTCTGTCAATATTT  
 TGATGCCACAATAAATTTGATTTTTTTTTACATTCCTTTTATTTTCTCTTAATTTAATTTGTTTATATAA  
 GCCTATCGTTTACCATTTTCAATTTCTTACATAAGTACAAGTGGTTAATGTACACACATCTTCAGTATAGGCATT  
 TCTTCTTGAGTGTGCAAAATACAGCTAGTTACTGTGCCAATTAAGACCCAGTTGATTTCCACCCATCTGTTTCT  
 TCTTGGCTAACTCTGTACTTCTGCCTTTAATTTACTGGGCCCTTATTCCTTATTTCTGTGAGAAATATAGAT  
 GATATGATTTATACCTTTCAATATATATTTTCTCAGTTATACAGAAATTTCAATATCTGGGATATATGTAC  
 CATTGTCAGCTATGACTA**AAAT**TTTGAAAAAGATAAAATTTCTAGCAAGCCTTTGAAGTTTACCAAGTATAGTC  
 ACATTCAGTGACAGCCCATTCATTCAGTAAGAATCATTTCAATCACCTTTGGGAGAGGCTATAATTACATTTA  
 TTGCAATGTTTCTCTTCTGCTAGATGTTACATAGCTCCCATTCTGTGGTTTGGCTTACAGCATATGTAACCA  
 AGGTTAGATGCCAGTTAAATTTCTTGAAGAAATGGATGAGCCTTGAGATTCTTAAGCTGGGACATGACATTT  
 TCTAGCTCTTTATCAGAATAACCAATTCACCTTTTTTAACTCGCACTTTTGACTTTTTTATGGTATAAAAA  
 CAATTAATTTATAACACATAAAGCTCACTGTGTTTTTAGACTTTTGATATTTTGTACTGTACAAACCTTTAT  
 AAATCAAGATGAAGACCTACAGGACAGATTCCCTTCAGTGTTTACATCAGTGGCCTTGTATGCAAAATATGCTGT  
 GTTGACCTGGACCTATAACTTTTGTAAAGACCTTGGAAATGTGGACATAAGCTCTTTCTTCCCTTTTGTGTAC  
 TGTATTTAGTTTGTGATAAATTTTCACTGTGGATATTTATGCTCTAAATCACTACACAAATCCCATATTA  
 TATACATTTGACCTGAAAAAAA

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**FIGURE 114**

MALERLCSVLKVLLITVLVVEGIAVAQKTQDGQNIGIKHIPATQCGI WVRTSNGGHFASPNYP  
DSYFPNKECIYILEAAPRQRIELTFDEHYIIEPSFECRFDHLEVRDGPFGFSP LIDRYCGVKS  
PPLIRSTGRFMWIKFSSDEEGLGFRAKYSFIPDPDFTYLGGILNPIDCQFELSGADGIVR  
SSQVEQEEKTKPGQAVDCIWTIKATPKAKIYLRFLDYQMEHSNECKRNFVAVYDGSSSIENLK  
AKFCSTVANDVMLKTGIGVIRMWADEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV  
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIIGITSGIVLVLLIISILVQVKQPRKKVM  
ACKTAFNKTGFQEVFDPPHYELFSLRDKAISADLADLSEELDNYQKMRRSSTASRCIHDHHC  
G  
SQASSVKQSRTNLSSMELPFRNDFAPQPMKTFNSTFKKSSYTFKQGHECFEQALED RVMEEI  
PCEIYVRGREDSAQASISIDF

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 348-369

**N-glycosylation sites.**

amino acids 311-315, 385-389, 453-457, 475-479

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 426-430, 479-483

**N-myristoylation sites.**amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,  
348-354, 352-358, 441-447

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**FIGURE 115**

GGTCTCTGCTCTGGCTGTGGCTCCTGCGCTCTGGCTGAGCCATGTTCTTCTCCTCGCCCTC  
CTCACTGAGCTTGGAAGACTGCAAGCCACGAAGTTCTGAAGGAATATTTCTGCATGTCACA  
GTTCCACGGAAGATTAAAGTCAAATGACAGTGAAGTTTCAGAGAGGAAGATGATTACATCATT  
ACAATTGATGGACAACCTTACACTCTACATCTCGGAAAACAATCATTTCTTACCCCGAAGCTTT  
TTGGTTTATACATATAATGAACTGGATCTTTGCATTTCTGTCTCCATATTTTATGATGCAT  
TGCCATTACCAAGGATATGCTGCCGAATTTCCAAATTCATTTGTGACACTCAGTATATGTTCT  
GGTCTCAGGGGATTTCTCCAGTTTGAAAAATACAGTTATGGAATTGAACCAAGTAGAATCTTCA  
GCAAGATTGAGCATATAATTTATCAAATGAAAAAATATGATCCAATGTATCCATTTTAGCA  
GTAATTTACAGTCATATTTGGCAGAAAAGACCAGCCCTACAAAGTTCCTTTAAACTCACAGATA  
AAAAATCTTTCAAAACTATTACCCCAATATCTGGAATATACATTATAGTGAAAAAAGCTTTG  
ATGTTTACCCAGTTCAAATTGACTGTTATACCTGTCCTTCTGGAATTGTGGTCAAATGAAAC  
CAGATTTCCACCAGTGGGGATGCTGATGATATATTACAAAGATTTTGGCATGGAAACGGGAC  
TATCTCATCTACGGCCCATGACATAGCATACTTACTTGTTCAGGAAACATCCTAAATAT  
GTGGAGCAACATTTCTGCGACCGTATGCAATAAAAGCTATGATGCAGGTATGCTATGTAT  
CCAGATGCAATAGGTTTGGAGGGATTTTCGGTTATTATAGCTCAACTGCTTGGCCTTAATGTA  
GGATTAACATATGATGACATCACTCAGTGTTTCTGCTGAGAGCTACATGCATCATGAATCAT  
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTTTAGCAACTGCAGCATGCACGACTATAGATAT  
TTTGTTCCTAAATTTGAGACTAAATGCCTTCAGAAGCTTTCAAATTTGCAACCATTACATCAA  
AATCAACCAGTGTGTGTAATGGGATTTTGGAAATCCAATGAAGAATGTGACTGTGGTAATAAAA  
AATGAATGTCAATTTAAGAAGTGCTGTGATTATAACACATGTAAGTGAAGGGCTCAGTAAAA  
TGTGGTTCTGGACCATGTTGTACATCAAAGTGTGAGTTGTCAATAGCAGGCACTCCATGTAGA  
AAGAGTATTGATCCAGAGTGTGATTTTACAGAGTACTGCAATGGAACCTCTAGTAATGTGTT  
CCTGACACTTATGCACTGAATGGCCGTTTGTGCAAGTTGGGAACGCCTATTGCTATAACCGA  
CAATGTCAAACACTACTGATAACCAGTGTGCCAAGATAATTTGGAAGGTTGCTCAAGGTGCTCCA  
TTTGCCCTGTTTAAAGAAGTTAATTTCTGCTGCAATGAAGATCTGAAACCTGTGGTTTAAATAAT  
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTCTGTGGAAATTAGCTTGTGTTAGCCA  
CATAAAAATGCTAATAAAAGTGACGCTCAATCTACAGTTTATTCATATATTCAAGACCAGTGA  
TGTGATCTATAGCCACTGGTTCCTCCATGAGATCAGATGGAACAGACAAATGCCATGTGGCT  
GATGGCACCATTGTGGTCCAGAATGTACTGTGTAATAAAACCTGCAGAAAAGTTTCATTTA  
ATGGGATATAACTGTAATGCCACCACAAAATGCAAAGGGAAGGATATGTAATAATTTTGGT  
AATTGTCAATGCTTCCTGGACATAGACCTCCAGATTGTAATTTCCAGTTTGGTTCCCCAGGG  
GGTAGTATTGATGATGGAATTTTTCAGAAATCTGGTGACTTTTATACAGAAAAGGCTACAAT  
ACACACTGGAACAACCTGGTTTATTTCTGAGTTTCTGCATTTTCTGCCGTTTTCATAGTTTTC  
ACCAGTGTGATCTTTAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAATGCAGAGTAT  
AATCGTAATTCATCCGTTGTATCAGAAAGCGATGACGTGGGACATTAATTTGACAGAACTT  
CCATAGCAATAAACCATAAGGAACGAATGTGCTTTATTTATAACCTTACGTTATCCCCAATGC  
ATTGTAATGTCAAACCTTTTGGAAATAAAGCTGCGTGCCCTCCC

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**FIGURE 116**

MFLLLALLTELGRLLQAHEGSEGI FLHVTVP RKIKSNDSEVSEKMIYIITIDGQPYTLHLGKQ  
SFLPQNFLVYTYNETGSLHSVSPYFMMHCHYQGYAAEFPNSEFVTLISICSGLRGFLQFENISYG  
IEPVESSARFEHIYQMKNNDPNVSILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY  
IIVEKALMFTQFKLTVLSSLELWSNENQISTSGDADDILQRFELAWKR DYLLLRPHDIAYLLV  
YRKHPKYVGATFPGTVCNKSYDAGIAMYPDAIGLEGFSVIIAQLGLNLVGLTYDDITQCFCRLR  
ATCIMNHEAVSASGRKIFSNCSMHDYRYFVSKFETKCLQKLSNLQPLHQNQPVCGNGILESNE  
ECDCGNKNECQFKKCCDYNTCKLKGSVKCGSGPCCTSKCELSIAGTFCRKSIDPECDFTEYCN  
GTSSNCVPDTYALNGRLCKLGTAYCYNGQCQT TDNQCAKIFGKGAQGAPFACFKEVNSLHERS  
ENCGFKNSQPLPCRKDVLCGLKACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG  
TDNAYVADGTMCGPEMYCVNKTCKRVHLMGYNCNATTKCKGKGICNNFGNCQCFPGHRRPDCK  
FQFGSPGGSIDDGNFQKSGDFYTEKGYNTHWNNWFILSFCIFLPPFFIVFTTVIFKRNEISKSC  
NRENAEYNRNSSVSVSESDDVGH

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 665-684

**N-glycosylation sites.**amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,  
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,  
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

**N-myristoylation sites.**amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,  
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,  
616-621, 634-639**Amidation site.**

amino acids 328-331

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**FIGURE 117**

CCCACGCGTCCGCGGACGCGTGGGGCTCAGTGGGCGTCGCGCGAAGGCTAAGGGAGTGTGGCG  
GGCGGCTCCGGGAGCCAAACATGCCTCGGTATGCGCAGCTGGTCATGGGCCCCGCGGGCAGCGG  
GAAGAGCACCTACTGTGCCACCATGGTCCAGCACTGTGAAGCCCTCAACCGGTCTGTCCAAGT  
TGTAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGTGATGGCTGACATCCGGGAAC  
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTCCGTCCCAACGGAGGATTGGT  
ATTTTGCATGGAGTACTTTGCCAATAATTTTGACTGGCTGGAGAAGTGTCTTGGCCATGTAGA  
GGACGACTATATCCTTTTTGATTGTCCAGGTGAGTTGAGTTGTACACTCACCTGCCTGTGAT  
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTTCCGAGTCTGTGGAGTTTTTCTTGTGTA  
TTCTCAGTTCATGGTGGAGTCATTCAAGTTTATTTCTGGCATCTTGGCAGCCCTGAGTGCCAT  
GATCTCTCTAGAAATCCGCAAGTCAACATCATGACAAAAATGGATCTGCTGAGTAAAAAAGC  
AAAAAAGGAAATTGAGAAATTTTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG  
TGACTTAAGAAGCAAAAAATTCAAGAACTGACTAAAGCTATATGTGGACTGATTGATGACTA  
CAGCATGGTTCGATTTTACCTTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA  
GCATATTGATTTGCCATTCAATATGGAGAAGACCTAGAATTTAAAGAACCAAGGAACGTGA  
AGATGAGTCTTCTCTATGTTTGACGAATATTTTCAAGAATGCCAGGATGAATGAAGAGTTTA  
CTAAAAGTAACCATCTAAAGAGCTTGTGGCCAAACCAGCAGAACATTCTTCTCTTCAAAGGAT  
GCAATAGTAGAAAGCTACTTATTTTAATGAAAAAAAGTAAACTTCGTTCTTTATCAGCCTCA  
TGCTGAATCAAATTTTAAATTATTTCTGAAACTGCTGCTGTTTAAAGTGAATCTTTTAGTAT  
TATAACAGCATCACTTTAGATTTTGTAAGTCAAAATTGAATGAATGCACATAGATTTATATA  
TAAATTAGCACCTGAGCTAAGGTTAAGGCCGGTCTAAACTTATTTTCACTTTTTGTATTATTT  
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGAAAAAGCTGCAAGGATAT  
ATATAAGACCACTGCTTATCTGTATCTTCCCATTTTCTATATTGAAAATGTATATTATTTAT  
ATAACTTAAAAAGTAAAAATAACTATGTTTTGAGAT

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**FIGURE 118**

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV  
MEDDSLRFPGNGGLVFCMEYFANNFDWLENC LGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ  
LEQWEFRVCGVFLVDSQFMVESFKFISGILAAALSAMISLEIPQVNMIMTKMDLLSKKAKKEIEK  
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRFLEPYDQSDDEESMNIVLQHIDFAI  
QYGEDLEFKEPKEREDESSMFDEYFQECQDE

**Important features of the protein:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 151-170

**N-glycosylation sites.**

amino acids 31-35, 47-51

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 212-216

**Tyrosine kinase phosphorylation site.**

amino acids 189-197

**N-myristoylation sites.**

amino acids 13-19, 76-82, 154-160

**ATP/GTP-binding site motif A (P-loop).**

amino acids 10-18

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**FIGURE 119**

GGGCGCTGGGAGACACCGGACGCCGCTCGGCTGCGCTGCGGCTCAGGCCCCCGCTCGGGCCC  
GACCCGCTCGGTACCGCCGGCTCGGGCGCGCACTGCCGCTCGGGCCCCAGGGCCATGCGG  
AGGCCACGAGAGGGCCGGCGGCCACGCGCATCCCGTAGCCAGGTGGGCCAGGTCTGCACCG  
CGGGCGCTCGGCGCC**AT**GGAGCCCCGTATTGCTGACGGCGCACTACGATGAGTTCCAAGA  
GGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGCGCGCGGGGCCCTCCCTGCCCCCGGCGCTT  
CCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCGGTCCGGGCTGCCGCGCTGGAACCGGGCG  
CGAGGTGTGCTGCTGCTGCGGGCTGGTGTTCGCCGCCGGCTCTCGCGCACTTCTGGCGGCTAT  
GCTGCCCTCAAGTACCTGGGCCCGGTGCGGGCGGGCGGGCGCTGTCCGAGGGGTGCC  
TGAGCGCAAGGCTTCGCGCGCGCGCTCGCTTCCTGGCGGCCAACCTGGAGCCAGCATCGA  
CCCATGCCAGGACTTCTACTCGTTGCGCTGCGCGGTTGGCTGCGCGGCCACGCCATCCCGA  
CGACAAGCTCACCTATGGCACCATCGCGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG  
CCTGCTGGCGCGGGCCGGGGTGGGCTGGCGCGCGGGCCAGCGCAAGGTGCGCGCTTCTT  
CCGCTCGTGCCCTGACATGCGCGAGATCGAGCGACTGGGCGCGCACTGCTAGAGGTGAT  
CGAGGACTGCGGGGCTGGGACCTGGCGGCGCGGAGGAGCGTCCGGGGTTCGCGCGCGCATG  
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCGCGCGCTCTTCTCGCT  
CAGCGTCACTGGGACGAGCAAGCACTCTCGCGCTACGTCATCCGCACTTGACCAAGGATGGGCT  
CACCTGCGCAGAGAGGACCTGTACTCTGCTCAGGATGAGGACAGTGAGAGATCCTGGCAGC  
ATACAGGGTGTTCATGGAGCGAGTGCTCAGCCTCCTGGGTGCGACGCTGTGGAACAGAAGGC  
ACAAGAGATCCTGCAAGTGGAGCAGCAGCTGCGCAACATCACTGTGTGACAGATGACGACCT  
ACGCGAGATGTCAGTCTCTGTACAACAAGGTGACGCTGGGGCAGCTGCAGAAGATCACCC  
CCACTTGGCGTGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTCTCAGAGGAAGGA  
GGTGGTGTCTGCTGGCGACAGCATACATGACGAGGTGTGCGAGCTCATCGCTCCACGCCCA  
CCGGTCTCTGCACAACCTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCC  
GCCATTCGCTGAGGCACTGCACGAGCTGGCAGGAGATGGAGGGCAGCGCAAGCCACAGGA  
GCTGGCCCCGGTCTGCTTGGGCCAGGCCAATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTT  
TGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGACGAGCTAGTGGAGACATCAA  
GTACATCTTGGGCCAGCGCTGGAGGAGCTGGACTGGATGGACCCGAGACAGGCGTCTGCG  
TCGGGCCAAGCTCCGATACATGATGGTGTGCTGCGCTACCCGGACTTCTGCTGAACCCGA  
TGCTGTGGACAAGGATATGAGTTTGAAGTCCATGAGAAGACCTACTTCAAGAACATCTTGAA  
CAGCATCCCTTACAGCATCCAGCTCTAGTTAAGAAGATTGCGCAGGAGGTGGACAAGTCCAC  
GTGCTGCTCTCCCCACAGCGCTCAATGCGCTACTATCTACCCAACAAGAACCAGATGGTGT  
CCCGCGGGGCTCCTGACGCCACCTGTACGACCTGACTTCCACAGCTCTCAACTACGG  
GGGCTCGGCACCATCTGGACATGAGCTGACCCAGGCTACGACAGTGGGGGGCCAGTA  
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCTCCTACAGCGCTTCTGCGAAA  
GGCTGAGTGCATCGTCCGTCTATGACAACTTCACTGTCTACAACACGGGGTGAACGGGAA  
ACACAGCTTGGGGAACATCGCAGATATGGCGTCTCTCAGTGGCTACCGACCTACCTATCA  
GAAGTGGGTGCGGGACGACGGCCAGAGCACCCACTTCCCCGGCTCAAGTACACACATGACCA  
GCTCTTCTTATTGCTTTTGCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT  
GCAGGTGCTACTGACAAGCATGCCCTGAGCACTACAGGGTGTGCGGCACTGTGTCCAGTT  
TGAGGAGTTTGGCCGGGCTTTCACCTGTCCCAAGGACTACCCATGAACCTGCCCCACAAGTG  
TTCGCTGTGG**TGA**GCTGGCTGCCCGCTGACGCCCCCACTGCCCCGACGAATCACTCTCC  
TGTGCTACCGGGCAGGATGCACCCGGTGCCAGCCCCGCTCTGGGCACTGCTGCTTCC  
AGCCCCCAGGACCCGGTCCCCCTGCTGCCCTCACTTCAGGAGGGGCTGGAGCAGGGTGA  
GGCTGGAATTTGGGGGCTGTGAGGGAATATAGTGGGTCCCCAGATTCTGCTCTAAGGGG  
CCAGACCTCTGCCAGCTGGATTGTACGGGCCCACTTCGCTGTGTTCTGCTGCAAGTCT  
TGGTCAATAAATCACTGCACTGTTAAAAA



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**FIGURE 120**

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL  
 SGLVFAAGLCAI LAAMLALKYLG PVAAGGGACPEGC PERKAFARAARFLAANLDASIDPCQDF  
 YSFACGGWLRRAIPDDKLTGYGTIAAIGE QNEERLRRLLARPGGGPGGAQRKVRAFFRSCLD  
 MREIERLGFRPMLEVIDCGGWDLGGAEE RPGVAARWDLNRLLYKAQGVYSAALFSLTVSLD  
 DRNSSRYVIRIDQDGLTLPERTLYLAQDE DSEKILAA YRVFMERVL SLLGADAVEQKAQEILQ  
 VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLKITPHLRWKWLLDQIFQEDFSEEEVLLA  
 TDYMQQVSQLIRSTPHRVLHNYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVC  
 LGQANRHFGMALGALFVHEHFAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAAARAKLQ  
 YMMVMVGYPDFLLKPAVDKEYEFEVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLLPP  
 QALNAYYLFNKNQMVFPA GILQPTLYDPDFPQSILNYGGIGTIIGHELTHGYDDWGGQYDRSGN  
 LLHWTEASYSRFLRKAECIVRLYDNFTVYNQRVNGKHTLGENIADMGVLKLAYHAYQKWVRE  
 HGPEHPLRLKYTHDQLFFIAFAQNWC IKRRSQSIYLQVLTDKHAPEHYRVLG SVSQFEFEGFR  
 AFHCPKDSMPNPAHKCSVW

**Important features of the protein:****Transmembrane domain:**

amino acids 64-88

**N-glycosylation sites.**

amino acids 255-259, 322-326, 656-660

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 722-726

**N-myristoylation site.**amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,  
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

**Prenyl group binding site.**

amino acids 772-777

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 609-619

**Neutral zinc metalloproteinases, zinc-binding region proteins.**

amino acids 609-619

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**FIGURE 121**

CGGACTGCCCGGACCGCGCG**ATG**GAGTGCAGCCGGCAGCGCTCGGGGAGGCCCGGGCGGACCCC  
GGGTGCTGCTGTTGGCGGGCGCATCGCGGGGCTGGCGCGCGCGCAGAGGCTCTGCGGCCACT  
CCGCTTCCCGACCTGCGGGTCTTGGAGGCCACGGCCCGCGCGGGGCGCGCATCCGCTCGG  
AGCGCTGCTTCGGTGGCGTGGTGGAGGTGGCGCGCGCTGATCCATGGGCCCTCCCGGGGTA  
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGGCTGCTGGGGGAGAAGGAGCTGTCCAGGAGA  
ACCACTGGTGGAGACCGGGGTCACGTGGGCTGCCCTCCGTGAGCTACGCCAGCTCCGGGG  
CCAGCGTGAGCCTCCAGCTGGTGGCGGAGATGGCGACTCTGTTCTACGGCCTGATAGACCAGA  
CCCGGGAGTTCTTGCACGCTGCAGAGACCCCGGTGCCAGCGTCGGGGAGTACCTCAAGAAGG  
AGATTGGCCAGCAGCTGGCGGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCCG  
TCCTGAACCTCCTTCTTCAACCTGGAATGCTGTGTGAGCGGCACCCACAGCATGGACCTGGTGG  
CCCTGGCACCCCTTTGGGGAGTATACCGTGCTGCCGGGGCTGGACTGCACCTTTTCTAAGGGCT  
ATCAAGGACTCACAACCTGCATGATGGCCGCCCTGCCGGAGGACACTGTAGTTTTTGAAGAAGC  
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGACAGCCTTTCCCGGGGAGACCTTTT  
CAGTGTCCGGTAGAGTGTGAGGATGGAGACCGGTTCCCGGCGCACCATGTGCATCGTACCGTGC  
CCTTAGGTTTTCTTAGGGAACATTGGACACCTTCTTTGACCTCCCTGCCGGCTGAGAAGG  
CAGAAGCAATCAGGAAGATAGGCTTTGGGACCAACAACAAAATCTTCTCGGAGTTTGAAGAGC  
CCTTCTGGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGGAGGACAGCTCGCCCTGGAGG  
ATGCTGCCCCTGAGCTACAGGACGCTGGTTCGGAAGCTCATTGGCTTTGTGGTCTGCGCTG  
CCTTTGCGTCTGTCCAGTTCTCTGTGGGTTTATTGCCGGACTTGAGTCTGAGTTTCATGGAGA  
CTCTGTCCGATGAAGAAGTACTTCTGTGTCTCACCAAGTGCTCCGGAGAGTGACAGGAAACC  
CACGGCTCCCCGCGCCCAAGAGCGTCTGCGGTCTCGCTGGCACAGCGCCCGTACACTAGGG  
GGTCTACAGCTACGTGGCCGTGGGCGAGTACTGGGGGCGACCTGGACCTGCTGGCTCAGCCCC  
TCCTGCAGACGGCGCGCGGCCAGCTCCAGATCCTGTTTGGGGGGAAGCCACACATCGCA  
CGTTTTACTCCACGACGCACGGGGCTCTGCTGTGCGGATGGAGGGAGGCCGACCGCCTCTCA  
GTCTGTGGGCCCCGAGGTGCAGCAGCCCAGGCCGAGGCTC**TAG**CTGGGCCCAGCCTACTCTG  
TTCCACCCGTGTCGGGGGTAGGCTGGGACCGTCATTCTTCTGACAGATTTCACTCTGGCTTG  
AAATTTGGGATGTTAATGAGGGTCTCTGTTTTTGGTAACAGGGCCACCTTCTCAGTTCT  
TGCTGTGTTATTGGAGTCTGGCCAGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA  
TGCTGGACACATAAAGCAAGTTACAGCCACAAAAA

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**FIGURE 122**

MESTGSGVEAPGGPRVLVVGGGIAGLGAAQRLCGHSAPPHLRVLEATARAGGRIRSERCFGGV  
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQENQLVETGGHVGLPSVSYASSGASVSLQL  
VAEMATLFYGLIDQTRREFLHAAETPVPSVGEYLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN  
LECCVSGTHSMDLVALAPFGEYTVLPGLDCTFSKGYQGLTNCMMALPEDTVVFEKPVKTIHW  
NGSFQEAAPFGETFPVSVECEDGDRFPAHHVIVTVPLGFLREHLDTFDPPPLPAEKAEAIRKI  
GFGTNNKIFLEFEEPFWEPDCQLIQLVWEDTSPLEDAAPQLQDAWFRKLIGFVVLPAFASVHV  
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA  
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV  
QQPRPRL

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 364-385

**N-glycosylation site.**

amino acids 253-257

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 408-412

**N-myristoylation sites.**

amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,  
216-222, 227-233, 443-449, 484-490

**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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**FIGURE 123**

CGGACGCGTGGGGGAAGATGGATAAATAATTCTGTACACGTCGCCCTGGCCCTCTGGAGCTCAGCTGCCAGTCCAC  
 GTCTAGGGAATCTTAGCACTCTGGGACCAAGACACTTTACAGCAATCATACCCCTTTGCAGAGGAGGTGAGCTCAC  
 CAGGACTCTGCTCCATTTTACAGCTTTTGTGCTACTGCCAGGTGGCCCCCACTGCTGACCGAGAGAGTGGTGGGA  
 TCTCTCAGTCTCCGCCGATCCCTGAAGCCAGTATCGCTGACCAGCAGCTCTTGCTTCTCTCAGCTACCTCTCTCT  
 CCTTCAGCTTGGGAGCCGAGCTCAGAGGTCARAGGTCTAGGCCCTGAGTATCCCATCTGCTGGCCCTCTGGCCGGGA  
 GAGGTGGAGTTCCTCGGCCACCTATGGCCACAGCTGGATGCCAGCAATGGAGATCCGCTGGTTCCGGAGTCA  
 GACCTTCRATTTGGTACACCTGTACCGAGGAGCAGCAGAGCTCCCTGGCAGGCGAGATCGCCGGCTCTCCGGAACAG  
 GACCAAGTTGATCAAGGACGACATCGCCTATGGCAGCGTGGTCTGCAGCTTCACAGCATCATCTCCCTCTGCACAA  
 GGGCACATATGGCTGCCGCTTCCACTCCGACAACCTTCTCTGGCGAAGCTCTCTGGAACTGGAGGTAGCAGGGCT  
 GGGCTCAGACCTCTCACCTCTCCCTTGAGGGCTTCAAGGAAGGAGGCATTACAGCTGAGGCTCAGATCCAGTGGCTG  
 GTACCCCAAGCCTAAGGTTTCACTGGAGAGACCCAGGAGCAGTGGCTGCCTCCAGAGTTTGAAGCCATCGTCTG  
 GGATGCCCAGGACTGTTCACTCTGGAACATCTGTGTTGTCCGAGCGGAGGCCCTCAGCAATGTGTCCGCTCTC  
 CATCCAGATCTCTCTTGAAGCAGAAAGAGTGTGGTGGTCAGATAGCAGAGCTGTTCTGATCCCGGAGCCCTC  
 TGGCTGGAAAGCGGCTTCTGCGGACCTGCGCGTGTCTGTTGGTCTCGCGCGCTGGCGCTGGCGCTCTCCG  
 GAAGCAGCGGAGAACCGGAGAAAGCTCAGGAAGCAGCGGAGAGAGCAAGAGAAACTCCTGCAGAGCTGGA  
 AAGCTTCAGACAGAGCTTGACTGGAGACGGCTGAAGCCAGGCTGAGTGGAGAGCAGGCCAAATATGCACT  
 GGAATGTAGCGCTGGACCGGCTCGCGCCACCCAGCTGGAGGTGTCCGAGAGTGGCAAGAGCTGTCTTCCCG  
 CGGGGCGCGGCGAGGCCGCGGCTGCGCCACCCGACAGCGGTTCTCGGAGCAGCTGCTGGCGCTGAGCCTGGAGG  
 GTTCTCCGCGCGCCCACTACTGGAGGTGCACGTGGGCGCGCGAGCGGCTGTTCTCTGGCGGCTGCTGCTGGC  
 CGCGTGGCGGCGCGCGGCGCTGCGCGCTGAGCGCTGCGCGCGCTACTGGGTGCTGGGCTGTGGAAACGGCTG  
 CGAGTACTTCTGCTGGGCGCGCACCGCTCGCGCTACCCCTGCGCGTGGCCCCGCGGCGCTGCTGCTCTCT  
 GCACTACGAGGCGGGAGAGCTGCTCTTCTCAACGTGTCCGAGGCTCCACATCTTCACTTCCACGACACCTT  
 CTCGGGCGCGCTCTGTGCGTACTTCAGGCCAGGGGCCACGACGGCGGCAACATCCCGGATCCCTGACCATCTG  
 CCGGCTGCGGCTTAGAGGAGCAGGGCTCCCGAAGAGAACGACAGTGACACTGGCTACAGCCCTATGAGCCCGC  
 GGAACCGCCCTGGACTGGTGCTGAGGCGCCCTCGTGGCGCGGACTGCGCCCGGGGGCCCTTGGATCTCCAG  
 GCCAGCGCTTGGCTCTCTGCTCGCTGTGAAGGGAGCAGGTGCACACGCCAAATGTGACGAGGGGGACAAAGA  
 GAGGGACCTTTGCCCTACGTAGATGTGTATGTGTAGTGGGATTTCTTCAAGGAAAGGAGCAAGTCCAAAGCTCG  
 TTTCTGGATTTGTGGGACTGAGCGAAGGAGTACAAATATATCCACGTCGCTCAGAGCTGGGCTGCTCAGGTTGGC  
 GGTGGGCAAGAGCCAGCATGGAAGAAAGAGGGAGAAACCTTTGGTGACTGCCCTAGAGGGATCAGTTAATTTG  
 TATAGTTTTATATTTTTTGTATATGTTTGCTAGCTCTAAGAGGTGCGATGCAATAACACTTCGTAAAGCAACGA  
 GTTCACTTAAGTAGGCTCAGATCCTAGTTTTAAAAACCATTTCCCATTAATAATGAAGTTGGAGGAACAGCTGCT  
 TCTCAGCGCGGGGCAAAATTTCAAGGTGAGCCTGGAGCATTGTGTGTGGTGAATATAAAGGCTCAAAAGCT  
 CAGCGCAACCCGGCAAAAGGTTAGGGAGCCAGGCGCGAAGGGGCTCACTGACCAATTTGGGCAATTTGAACAT  
 CAGGATGAATAAGACAGGAGAGATTATAACACACTGAATAAAAAACATATCCATGAGTTCTATGCTGATACTCAA  
 ATTCTTTTTAAAAAGGACAAACAGGAAGTTTCTTTGGAGGTGAATCTAATATTGGTGAGAGTCTTGGAGA  
 ACAGGCTGTTCCAGCTCAAAAGCATACCTTATACACTCTATAAGTTGAAGGGGAAGGTTACCTTTAC  
 ATTGGAGACATCTACAGATCATCCAGTGATTAATTTAAATCATCATCAATGATGGGACCAAGCATTATTTAGT  
 TTGACAACTGGGGAAGAAGTGTCTTCAACCCCTACCCCGAAGACATCTCTCTGTGGCGCAGGCTGGAGTGCA  
 GCTCTCAACCTCTGGGCCAAGTGATCTCCACCTCAGACACACAACACCAAGGCCCAATTTAAGTGGATTAG  
 AGACGGGGGTCTCACTTTGTTACCCAGGCTGGTCTCAAACTCCCTGGCGTCAAGCAATCTCTCCACCTGGGGCTCC  
 CAAATGCTGGGTGTACAGGCATGAGCCGCTGCTGCTGGCTTCATTTTCAGATGAGACATTTGTACTGTGGCTA  
 GTGAGAGAACATTTCTGTTCTTAGCAACATACTGAAGTTTGTAGATATTAATACACAGTGTCTGCCACTGA  
 ATTTCCAGTGACTAAGTGGAAAAATATAAACATATGAATATAAAGAAAGGAAGACAAGTCAAAATGTAGTAAA  
 ATGACAACACTGGTGACTCTAGTGACTGGTGCAGAGATGTTCAATGTACTATCAATGTGGCTTTGGCTGGGT  
 TTTGAATTTTCAAGTCAAGGCTGGGTGGCGGAGAGGATACCAAAAAACATAAGTGAATATCTTTGGATG  
 GGAAATGTTTGGTAATGCAATCTTAAATGCTCTCTTTGATTTTTTAAATGTCAATATATGATATGATCAG  
 TTCTGTATTAAGGGGGAACACCTTTTCA

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**FIGURE 124**

MVDLSVSPDSLKPVSLTSSSLVFLMHLLLLQPGEPSSEVKVLGPEYPILALVGEEVEFPCHLWPF  
QLDAQQMEIRWFRSQTFNVVHLYQEQQQLPGRQMPAFNRNRTKLVKDDIAYGSVVLQHSIIPS  
DKGTYGCRFHSDFNSGEALWELEVAGLGS DPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH  
QGQCLPPEFEAIVWDAQDLFSLETSSVVVRAGALSNVSVSIQNLLLSQKKELVVQIADVFPVPGA  
SAWKSAFVATLPLLLVLAALALGVLRKQRRSREKLKQAEKRQEKLTAELEKLQTELDWRRAE  
GQAEWRAAQKYAVDVTLDPASAHFSLEVS EDGKSVSSRGAPPGPAPGHPQRFSEQTCALSLE  
FSAGRHYWEVHVGRRSRWFLGACLA AVPRAGPARLSPAAGYWVLGLWNGCEYFVLAPHRVALT  
LRVPPRRLGVFLDYEAGELSFNFVSDGSHIFTFHDTFSGALCAYFRPRAHDGGEHPDPLTICP  
LPVRGTGVPEENDSDTWLQPYEPADPALDWW

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 247-272

**N-glycosylation sites.**

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

**Tyrosine kinase phosphorylation site.**

amino acids 105-114

**N-myristoylation sites.**

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

**Amidation site.**

amino acids 390-394

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**FIGURE 125**

TATAGTCCCGACTACTCATGGGGCTGATGCAGGTTGAGGCAGGAGGTTTCATGAGCCAGGAGGTTGGAGCTGTAA  
 TGAGCTAGGATTTCTGCTCTGCATCTTAGCTGGATGACAGAGCAAGACCCCTGTCTCAAAAAGAAAAA  
 AAAAGAAATGCATGAACAGACATGACAGTTCTGGCCCTCAAAGATCTTCCAAAGAAATGATTTTTTTTAAAC  
 ACCAATCTGCGAGGAAAAGAACATATTTAAGTTATCCAAACACCTATCCAAATTTGTAAATCATTTATCAT  
 GACATGGTGAGATGTTGTTATATTTCTTTCTTTAGGTGAACACCACTTCAAAGTCTGAGTCAATCTCTTTCA  
 CCTAAAGAGTTGGTCCGGATACATGTCCCTAAACCTTTGGACAGGAATGATGGAACATTTTGTAGAGATATAG  
 ATGATGAACCTGTCAGTGAAGGCTCGAAGATAGAGGTCCTTTATGGTGATGAACATTTGGCTCAGTCTCCCTAT  
 ATTTTGAAGGACCAAGTGACCATGAGTACTGTAGTGTCCGGGAAGATCCTCAGGCTTGGCAGGAAGCTTTCT  
 TGTCCAACCAAGAACACAGATGTGAAAAGATTTTGTCTCTTCCAGCATCAATCTCCAGCAATGTCTAA  
 GAAGTCCCAAAAGGTTTGGGGATGAGAGAGGTGCCATTTGTTTACATACAGATTCTCAATAACCATGTTTACCGG  
 AGATCTTAGGGAATACACAGACTCAAGATGTTCTCTGATGAGATTTTGTATCATTGACAGGAAGGTCCCT  
 CTCCAGATTTAGAATTTTATGTTAATCTTGGAGTTGGCCCTTGGAGCATCGAAAAGTCAATGGAACCCCTAGC  
 CCGATACCTATCATTTCTGGTGTGGCTCTCTGGATCAAGAGATGTTGTCTTCCAACGTTATGACATCAACCCAC  
 TCCATGCTTGAAGCCATCGGGGTGTTACAAATGATCTCCTCTATTCAGGGAATACAGGGCTCTCTGGATC  
 AATAAACAGAGAGAGCTTTCTTCAGAGGTAGAGACAGCCGAGGAGAGGCTCCAGTTGGTACAGCTGTCCAAA  
 GAAATCTCAGCTACTAGATCGAGGAATACAGGATATTTCTTTCAAGAGAAAGAAAGAGCTTGGAAA  
 GCCAAGTTGATGGGTTCTTTGATTTCTTTAGTACAAGTATCAGTAATTTGGATGGGACCGTGGCTGCTTAC  
 AGATATCCATCTCTCATGCTGGGCGAGCTGTGGTTTAAAGCAGGACTCGCCATATTTAGAACATTTCTCATCTG  
 GCATAGAACCTTGGAGACCTATGTTTCCAAATTAAGAAATCTGAGTGATTTTATAGAGAAATTTAAATGGGCT  
 AAGGAAATGATGAAGAAGCCAAAGGATTTGCAAAAGAGGACAGTTGATGGCTAGGGCACTACAGCCACAC  
 AGGCTTTGATGCTAGTTTACCAGTACTCGAGAAATATCGCAGCGCCAGTCCAGCAACCCGAAGTACGTGAT  
 GAACTTTGAAGTCTGCTCCTCAGCCAGAGATAGCAGAGCATCTGCCAGTGCACAGGAAAGAGCTTCAAGGAGA  
 GAACTTTGAAGTCTCAGCCAGAACTACAGACTCTCTGTGATTCGCGCTACACTTTAAGGAAGATTTGAATCTAAGCTGT  
 GAAGGACAGTATAGAGAGCTGACCAAGTGGATAGTTCTCCGGTGGCTTTATATATGTAGATGATATAGCAG  
 TACTGGTTGAGTATCCCTCATCTGAATGCTTAGGACAGGAGTGTTCAGGCTTCAGATTTTAAAGTTTGGG  
 AATATTTGCATGTACATATAGAGGTATCTTGGGGATGAGATCCAGTCTAAACACAAATTCATTTATATTTAT  
 ATATACCTTGTTCACATACCTCGAAGGTAAATTTATATAATATTTTAATAATTTTGTGATGAACAAAGTTTGT  
 ATACATTTGAAGCTGCAGAAAGCAAGGTGTCACTATCTTAGCAGCCCAAGTGGTGGTGCAGCATCAAAAGTT  
 TTGGATTTTGGGTATTTAGATTTTATGATTTTGTATAGGAAATGTTCAACCTATGTTTGAACAGCACTATCA  
 AATATCATTTGAATTAATATCTTTTGGTAAAACTGCTATTTATCAGCATATGATTTCTCTAAAAGGAACTAC  
 TGGGATCATAGAGATAGAGAGACTTGTCAAAATATAAATCAGGCTCTCGCAAACTGTTTACATATTTATTTGT  
 TTACATATTTTATGGTTTATTTCTATCCCTGTTCACTTTTCTGCCATTTCCAAATCTCCAATTAAGAGAAATAT  
 TTGTTCAAGGTGTGTCGCCCGCGCCCGCTCACTGCATATTTCTCTTACAAGCTGCTTTTGGCTTTCTATTA  
 TAACAGCTTCCCTTTTAGAAGGCTGTGATAAGGATTTAAGGAAGAAGAGAAATGACTCTGTTTATTAAGGTGGCAT  
 GGAAGCTGTGGAGGGAATATTTTATAAGCACTACTCATATCTCTTAAACTAAATTTTGCAAAAGCCGAGACAA  
 CATTAAGGAGAATTTGACCTTAAGTTAGTAATTCMAATCTATCTGAGTTTATACCATCAAGACATCAAG  
 TTATTAACATAGATGAAGGTATGCTATAGGCACTATTCAATATCTCTATATTTGATAGGTGAAGATTAAGTGTAG  
 TCAGGTGAAGGAGCTATCATCATTTTAAAGCTGAAGAGGGGATCCTTGAAACAGTGAAGAACTCTACACAACT  
 TCAGAGAGCGTGTCTATTTGGGATCTCAATAATAGGCGCAAGAAAGGCAAGCACTCATTCTCACTCCAC  
 ACTTTTCTATTTGAGTGGGTGTCAATGCTACGATGAAGACTTTGGAAATTTCTCTTTTGAAGCAGGGTCA  
 GGATTTAGGACTCATAGCTGAAAGCTCATACACTCTTGTAAACATATGACTCCAGAGTTCAGTCACTAAAG  
 TGCATGTTTCTAAAGCAAGAGATTTCTCTCATTTCAAATTTTAAATATATGACTCTGGCCGGTTCAGTGGCTCAGC  
 CCGTAAATCCAGCACTTTGGCAGCGGAGATGGCGGATCTTTGAGGTCAAGGATTTTGACAGCAAGCTGGCCA  
 ACATGGTGAACCCGCTCTCTACTAAAAATCAAAAAATTAGCCAGGCACTGGTGGCATTTGCTCTGTAATCCAGCT  
 ACTCGGCTCTCTCGCAATCTCAGCCGACGCTTTAAAGAGTTAGTGTTAATGGCTTTCTGTGTTGAAGGACAAA  
 ATGCATCTATGTTGGTTGAAGATTTGGGAGGAGATTCACCAATATCTGAGGAGAGATGGATGAAGGAAATCTCT  
 ACTTTTGGCTTTATACCTTTCTATAATTTTATGATTTTCTTACTGTAAGTATGATCAAGTTGCAAAATTAAG  
 AAAATGCCAACCTTGAAGAAAGACATAAATGCAGAAAGATATAAACAGGAACAGCAATATTTATATTTTTC  
 ATTTTGTCTTTTAAATCTATGTTAGAACCTTATATCTTGGGACTATGATATATATACCTTTTAAATATAA  
 ATAAATTTCTTAATAAAAAGTTG

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**FIGURE 126**

MVELFIFLFLLLGETPFKVVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL  
YGDEHVAQSPLYLKGPVYHEYCECPEDPQAWQKTLSCPTKEPQIAKDFASFPSINLQQMLKEV  
PKRFGDERGAIVHYTILNNHVYRRSLGKYTDFKMFSDIILSLTRKVLLPDLEFYVNLGDWPL  
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLLSIQGNTGPSWINKT  
ERAFFRGRDSREERLQLVQLSKENPQLLDAGITGYFFQEKELGKAKLMGFFDFFKYKYQV  
NVDGTVAAYRYPYLMLGDSLVLKQDSPYYEHFYMALEFPWKHYVPIKRNLSDLLEKVKWAKEND  
EEAKKIAKEGQLMARDLLQPHRLCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC  
HRKKPSREEL

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 250-254, 363-367

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 444-448

**N-myristoylation site.**

amino acids 208-214, 319-325, 388-394

**Endoplasmic reticulum targeting sequence.**

amino acids 448-453

**Mitochondrial energy transfer proteins signature.**

amino acids 25-34

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**FIGURE 127**

AGCCGTCGGAGGGAGCCGGAGCGCTTCTCCCGAGTTGGTGATAGATTGGTGCTCATCCAACAT  
GCAGAAATGAATGAGCAGTGAAGCAGCAGAGCCGATGGGTGATGAGGATGTAAGTGCCTTT  
GAAGGCTTCCACACCTCTACTCCAGGAATCATGAATAAATGGAGGATAAGCAGGACCAGAT  
GATACCA**TGA**AGAGAAGTTTACAGGCCCTCTATTGCCAACTGTTAAGTTTCTGTCTGATCTTG  
GCACTGACCGAAGCGCTGGCATTGTCATCCAGGAACCATCTCCAGGGAATCTCTTCAGGTCT  
CTCCCTTCAGGCACCTCCCGGGGAACCATGGTGACAGCACCCACAGCTCTACCAGACATACT  
TCTGTGGTGATGCTGACCCCAATCCCGATGGACCCCTCACAGGCTGCAGCTCCCATGGCA  
ACACTGACACCCCGTGACAGAGGGGCACCTCTACGCACACCATCTCCACCATCGCTGCGACA  
GTAAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCGCCGCTCCAGCAGCCATGGCAACC  
ACATCTCCAAAGCCAGAGGGCGCCCTCGAGGGCAGGCTGCCCCACCATCTGTCTGACAAAG  
CCACCGGGGGCCACAGCGGCCCAACACAGCGCCCCCGCACTACCAACAGCAGGCCCCC  
AGGCCCCCAGGCTCTTCCCGAAAAGGGGCTGGTAATTATCACGCCCCGTGCCCGCTGCACCT  
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAATCCAAGTCCACACCTCTGGGG  
CAGAAGCGGCCCTGGGGAAAATCTTTAGATCTACAAGGGCAACTTCACAGGGTCTGTGGAA  
CCAGAGCCCTCTACCTCACCCCCAGGACCCCACTCTGGGGCTACTCTCTTACCACAGCCC  
CAGACATGGGTGCCACCACAGTGCCAGCAATACCTCATGGGGACCCACCACACCTCCCTG  
GGCCTGCAAAGGACAAGCCAGGCTTTCGACAGCAGCCAGGGGGGTGGTTCTACCTTCACC  
AGCCAAGGAGGGACACCAGATGCCACAGCAGCTCAGGTGCCCTGTGAGTCCACAAGCTGCC  
CCAGTGCTTCTCAGCGCCCCCACCACGGTGACCCACAGGATGGCCCCAGCCATAGTGACTCT  
TGCTTACTGTACCCCTGGCACCAGCAGACCTCTGTCTACAGCTCTGGGGTCTTACGGCT  
GCCACGGGGCCACCCAGCTGCCTTCGATACAGTGCTCTCAGCCCCCTCCAGGGGATTCT  
CAGGGAGCATCCACAACCCACAAGCTCCAACCCATCCCTCCAGGGTCTCAGAAAGCACTATT  
TCTGGAGCCAAGGAGGAGACTGTGGCCACCTCACCATGACCGACCGGGTGCCAGTCTCTC  
TCCACAGTGGTATCCACAGCCACAGGCAATTTCTCAACCGCTGGTCCCCGCCGGGACCTGG  
AAGCCTGGGACAGCAGGGGAACATCTCCATGTGGCCGAGGGGGACAAACCGCAGCACAGAGCC  
ACCATCTGCCTGAGCAAGATGGATATCGCCTGGGTGATCTCTGGCCATCAGCGTGCCCATCTCC  
TCTGTCTGTCTGTCTGACGGTGTCTGTCATGAAGAGGAAGAAGAACGCCCAACCCGGAG  
AACAACTGAGCTACTGGAAACAACACCATCACCATGGACTACTTCAACAGGCATGCTGTGGAG  
CTGCCAGGGGAGATCCAGTCCCTGAAACCTCTGAGGACCAGCTCTCAGAGCCCGCTCCCA  
GCCAATGGGCACTATAGAGACACTGGGATGGTCTTGTAAACCCCTCTGTCAAGAAACACTG  
TTGTGGGAAACAGATCAAGTATCTGAGATCT**TAA**CTCAGCAGGCATCACTTTGCCATTCCGTA  
TTTTTCGTCTCTAAATTATAAATATACAAATATATATATTATAAATATAACCTTGTGTAAAGCT  
TGACTTAATGAGAAACATTTTCAGCTTTTTTCCATGAAATGTACAACATCTTTTATCAAGT  
GTGGTTTAAAAAATAAATACTTTACAGAATGATCTGTGGCTTTATAAATAAAGGATATTCT  
AAGCAAAAAAAAAAAAAAAAAA



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**FIGURE 128**

MKRSLQALYCLLSFLLILALTEALAFAIQEPSPRESLQVLPSGTPPGTMVTAPHSSSTRHTSV  
VMLTFNPDGPPSQAAAFMATLTTPRAEGHPPTHISTIAATVTAPYSESSLSTGPAPAAAMATTS  
SKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRPFGSSRKAGNSSRPVPPAPGG  
HSRSKEGQGRNPSSTPLGQKRFLGKIFQIYKGNFTGSVEPEPSTLTPRTLPLWGYSSSPQPQT  
VAATTVPNSNTSWAPTTSLSLPAKDKPGLRRAAQGGGSTFTSQGGTTPDATAASGAPVSPQAAPV  
PSQRPHHGDPQDGPSHSDSWLTVTPGTSRPLSTSSGVFTAATGTPPAAFDTSVSAPSQGI PQG  
ASTTPQAPTHPSRVSESTISGAKEETVATLTMTRVPSPLSTVVSTATGNFLNRLVPAGTWKP  
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAI SVFISSCSVLLTVCCMKRKKKTANPENN  
LSYWNNTITMDYFNRAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFCQETLFV  
GNDQVSEI

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 469-487

**N-glycosylation sites.**

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 495-499

**N-myristoylation sites.**amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,  
288-294, 296-302, 351-357, 374-380, 427-433, 442-448**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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**FIGURE 129**

AGGCAGGGCGGGCGCGCTGCACACACGCACACGGAGCT**AT**GGGGTGCCATGTTGCCACCAG  
CTGCCACGTGGCCTGGCCTTTTGGTGCTGATCTCTGGATGCTGGGGCCAGGTGAACCGGCTGCC  
CTTCTTACCAACCCTTCTTTGATACATACCTGCTGATCAGCGAGGACACGCCCTGTGGGTTC  
TTCTGTGACCCAGTTGCTGGCCCAAGACATGGACAATGACCCCTGGTGTTTGGCGTGTCTGG  
GGAGGAGGCCTCTCGCTTCTTTGCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGCC  
ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTGACGGACACCAGGGGGT  
GATCACACGGGAAGGTGAACATCCAGGTCGGGGATGTGAATGACAACGCCGCCACATTTACAA  
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGGACGCCCATCTTCATCGTGAA  
TGCCACAGACCCGACTTGGGGGCGAGGGGCGAGCGTCTCTACTCTTCCAGCCCCCTCCCA  
ATTCTTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC  
CACACAGGCCTACCAGCTCAGGTCACAGCCACAGATCAAGACAAGACCAGGCCTCTGTCCAC  
CCTGGCCAACTTGGCCATCATCATCACAGATGTCCAGGACATGGACCCCATCTTCATCAACCT  
GCCTTACAGCACCAACATCTACGAGCATTTCTCTCCGGGCACGACGGTGCGCATCATCACCGC  
CATAGACCAGGATAAAGGACGTCCCGGGGCATTGGCTACACCATCGTTTCAGGGAATACCAA  
CAGCATCTTTGCCCTGGACTACATCAGCGGAGTGCTGACCTTGAATGGCCTGCTGGACCGGGA  
GAACCCCTGTACAGCCATGGCTTCATCCTGACTGTGAAGGGCAGCGAGCTGAACGATGACCG  
CACCCATCTGACGCTACAGTCACCAACGACCTTCAATATCCTGGTTATTGACATCAATGACAA  
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTCCGCTT  
TGCCCTTCCACTCTTCATCCAGGTGGTGGACAAGGATGAGAATTTGGGCTGAACAGCATGTT  
TGAGGTGTACTTGGTGGGAACAACCTCCACCACTTCATCATCTCCCGACCTCCGTCAGGG  
GAAGGGGACATTCGTATTCCGGTGGCCATCCCACTGGACTACGAGACCGTGGACCGCTACGA  
CTTTGATCTCTTGCCAAATGAGAGTGTGCCTGACCATGTGGGCTATGCCAAGGTGAAGATCAC  
TCTCATCAATGAAAATGACAACCGGCCATCTTCAGCCAGCCACTGTACAACATCAGCCTGTA  
CGAAGCTCACCCTGGGGACCTCTGTGCTGACAGTCCTGGTGAATCCCGCTTCACTGCAGG  
GCCACTGAGCTCCAGGGCCGACTGTGGTGAGGCACCCAGAGGGATTTGTCCAAGGGACCT  
CAGCAATCAGGGAAGGAGGCACCCCAATCCCTGAGCTGTGTTTGGTGGTGTAT**TAA**AATAAA  
GTTTTGGACTCTTCAGGAAGGGCTCCCTTGACCTAGGTTGCAATATGAAAAGGAGCCAACT  
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTCTCGCTTCCCTGAGAGAGACTCAG  
TGAGGGTGGGCTGGGAGCCCTGGAAGCCCCCTCAAATGGGTGGGAAGGTGCCAGCCATCCTTG  
AGAAGGGCAACCTCTCCATGTGAGCACAGGCACCAGAGAGGGGCGAGCGCCTGGAGGGTACC  
GGGACCCCAAGCTGCCATGGCTGGACTTGCCCTTGACAAGGGGCCCTCCCAAGTGTCTATT  
TGATCTGTCACTCTTGGTTGCAAGGGACAGAAACCCCTTAAGTAGTTCAAGCAAAAAAGG  
ATTGGCTCATGTAACTCAAAAGTATAAGTGATTTGAGCCCGGCTCGGTGGCTCAGCCTGTGC  
ATCCAACACTTGAGAAAGCCGAGGTGGGCGGATCACTTGAGGTGCGGAGTTTGAGACCAGCC  
TGGCCAACATGGCAAAACCCGCTCTCTACTAAAAATACAAAAATAGCCGGGTGTGGTGGCAC  
ACGCCTGTAGTCCAGCTACTAGGAGGCTGAGGCAGGAGATCGCTTGAACCCAGGAGCGG  
AGGTTGAGTGAAGCCAGATTTGTGTCCTGACCTCCAGCCTGGGGACAGGCCAGATTTCTGT  
CTC

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**FIGURE 130**

MGCHVATSCHVAWLLVLISGCWGVNRLPFFTNHFFDTYLLISEDTPVGSSVTQLLAQDMDND  
 PLVFGVSGEEASRFFFAVEPDGTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN  
 DNAPTFFHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV  
 IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG  
 TTVRIITAIDQDKGRPRGIGYTIIVSGNTNSIFALDYISGVLTNLGLLDRENPLYSHGFILTVK  
 GTELNDORTPSDATVTTTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE  
 NLGLNSMFEVYLVGNNSHHFIISPTSVQKGADIRIRVAIPLDYETVDRYDFDLFANESVPDHV  
 GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLVSPRFTAGPLSSPGPTVVRHP  
 EGFCPRDLNSQGRRHQPIPELCLLVY

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 355-374

**N-glycosylation sites.**amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,  
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

**Amidation site.**

amino acids 515-519

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**Leucine zipper pattern.**

amino acids 298-320

**PTS HPR component serine phosphorylation site signature.**

amino acids 377-393

**Cadherins extracellular repeated domain signature.**

amino acids 120-131, 336-347

**Cadherins extracellular**

amino acids 120-144, 336-360

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**FIGURE 131**

GTGGGCCGCCCTGCTGCTGCCGTCC**ATG**CTGATGTTTGGCGTGATCGTGCCCTCCAGCGGGC  
TGCTGCTCATGATCGAGCGGGGCATCCTGGCCGAGATGAAGCCCTGCCCTGCACCCGCCCG  
GCCGCGAGGGCACAGCCTGGCGCGGGAAGCCCCAAGCCTGGGGGCGTGTCCCTCAGGGGTG  
GGGACGCGGACTTGCAGTGCGGCAGGACGTCCGGAACAGGACCCTGCGGGCGGTGTGCGGAC  
AGCCAGGCATGCCCCGGGACCCCTGGGACTTGGCGGTGGGGCAGCGGCGCACCTGCTGCGCC  
ACATCCTCGTAAGTGACCGTTACCGCTTCTCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA  
ACTGGAAGCGGGTGATGAAGGTGCTGGCAGGCGTCTGGACAGCGTGGACGTCCGCCTCAAGA  
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTGCGTACCGCC  
TGCAGCACTACTTTAAGTTCTGTGTTGTGCGGGAGCCCTTGAACGCCCTCTCTGCTTACC  
GCAACAAGTTTGGCGAGATCCGAGAGTACCAGCAACGCTATGGGGCTGAGATAGTGAGGCGGT  
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCTCCGAGTTCTGAGAT  
ACCTGGTGGATGAGGACCCTGAGCGCATGAATGAGCATTGGATGCCCGTGTACCACTGTGCC  
AGCCTTGTGCCGTGCACTATGACTTTGTGGGCTCCTATGAGAGGCTGGAGGCTGATGCAATC  
AGGTGCTGGAGTGGGTACGGGCAACCACTCACGTCCGATTTCAGCTCGCCAGGCGCTGGTACC  
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGAGTGCCCCCGGGCCTGCTGCAGG  
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCTCTTTGCCCTACCCACTGCCTAATGTCACCA  
AGGAGGCGTGTGAGCAG**TGA**CCATGGGTGTGGGGCCAGCAGCTGGTGGGACTGGTTTCAACG  
CCAGCTTTCTGTGCTTCTGCCTGTCAATCGGAGAACTCTGGCTCTGGGGCTTGGGGCTTCTC  
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAAGTTCTTTGCCAGGGTGGGCACCCACAGTGA  
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCTCATTGGGGGATCTCTTGGGGGGCA  
GACACCAGTTTGCCAATGAAGCAACACATCTGATCTAAAGACTGGCTCCAGACCCCGGGCTGC  
CAGGATTATGAGTCCACTTGGTCTACCTTAATTTAACCTGTGGCCAAACTCAGAGATGGTAC  
CAGCCAGGGGCAAGCATGACCAGAGCCAGGGACCCTGTGGCTCTGATCCCCCATTTATCCACC  
CCATGTGCCCTCAGGACTAGAGTGAGCAATCATACCTTATAAATGACTTTTGTGCTTTCTGCT  
CCAGTCTCAAAATTTCTACACCTGCCAGTTCTTTACATTTTCCAAGGAAAGGAAAACGGAA  
GCAGGGTTCTTGCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCTCTGTGCC  
CAGCCTCTTCTTGAGTTCTCGGAACCTCCTCCCTAATTCTCCCTTCTTCCCCACAAGGCCT  
TTGAGGTTGTGACTGTGGCTGGTATATCTGGCTGCCATTTTCTGATGCATTTATTTAAATTT  
TGTACTTTTGTATAGAACCTTGTGAAGGCTTTGTTTTCTTAATAGCTGACTTTTTAATAAAG  
CAGTTTTATATAT

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**FIGURE 132**

MLMFAVIVASSGLLLMIERGILAE MKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ  
DVRNRTLRAVCGQPGMPRPDWDLVPGQRR TLLRHILVSDRYRFLYCYVPKVACSNWKRVMKVL  
AGVLDSVDVRLKMDHRSDLVFLADLRPEEI RYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE  
YQQRYGAEIVRRYRAGAGPSPAGDDVTFF EFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF  
VGSYERLEADANQVLEWVRAPPHVRFPARQAWYRPASPESLHYHLC SAPRALLQDVLPKYILD  
FSLFAYPLPNVTKEACQQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 67-71, 325-329

**Tyrosine kinase phosphorylation sites.**

amino acids 152-159, 183-183

**N-myristoylation sites.**

amino acids 89-95, 128-134

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**FIGURE 133**

CGGCAGTTTCTGGCCCTGCAGCTGGAGGTACCTGAGTTCTGAGGGTCGTAGTGCTGTTTCTG  
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTTGAATCAGCTTCTCCATG  
GCCTGGGGACCAGTTCCCGCTGAGCCATTTTCCTTTTGGCTAAAAGTCCCCGCCAGAGGCC  
AATTCGTGCGGCGCGGGTGGAGATCGCAGGTCGCTCAGGCTTGCA~~ATG~~GGTCAAGGGTTGT  
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGCTACAGTGAGCAAGGCTACCTCACCA  
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTTCTAACACCAATCATCGTAAACAGTCC  
AAGGAGGCATTGACATATATCATCTTTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA  
TTAATTTGGAAATGTTGCCTCCTGAGCTAAGCTTTACCATCTTGCCTACCTGAATGCAACTG  
ACCTTTGCTTGGCTTCATGTGTTTGGCAGGACCTTGCGAATGATGAACCTCTCTGGCAAGGGT  
TGTGCAAAATCCACTTGGGGTCACTGTTCATATACAATAAGAACCCACCTTTAGGATTTTCTT  
TTAGAAAATTGTATATGCAGCTGGATGAAGGCAGCCTCACCTTTAATGCCAACCCAGATGAGG  
GAGTGAACACTTTTATGTCCAAGGGTATCCTGGATGATTGCCAAAGGAAATAGCAAAGTTTA  
TCTTCTGTACAAGAACAATAAATTGGAAAAAAGTGAAGATCTATCTTGATGAAAGGAGAGATG  
TCTTGGATGACCTTGTAAACATTGCATAATTTTAGAAATCAGTTCTTGCCAAATGCACTGAGAG  
AATTTTTTCGTATATCCATGCCCTGAAGAGCGTGGAGAGTATCTTGAAACTCTTATAACAA  
AGTTCTCACATAGATTCTGTGCTTGCAACCCTGATTTAATGCGAGAAGTTGGCCTTAGTCCTG  
ATGCTGTCTATGTACTGTGTACTCTTTGATTCTACTTTCCATTGACCTCACTAGCCCTCATG  
TGAAGAATAAATGTCAAAAAGGAATTTATTCGAAATACCCGTCGCGCTGCTCAAAATATTA  
GTGAAGATTTGTAGGGCATCTTTATGACAATATCTACCTTATTGGCCATGTGGCTGCA~~TAAA~~  
AAGCACAAATGTAGGACTTCAGTTTTTACTTCAGACTAAAGCTACCCAAGGACTTAGCAGAT  
ATGGGGGTTACATCAGTGCTGGTCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC  
CTTTTTTCTTTTGCCATTTTCTATTTTAGTAATTTCTTGGGGAAGTAAATAATTTTGAGA  
ATTTTTCCTAATTTTGTATATCAGTTTTTGACAAAGCAGAGCCACTGTCTAACACAGCTGTT  
AACGAATGATAAAGTACATTATACTCTAAAAGATGGTGTATTTGTGCATTAGATTTGCCTGA  
AAAACCTTTATCCATTTCCTTTTATACAAATACCATGTAATGTGTACATATTTAACTAAAG  
AGATTTATAGTCATAATTATTTTATTGTAAAGATTTTAACTAAAGTTTTTCCTTTCTCTC

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**FIGURE 134**

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRMDASNISNTNHRKQVQGGIDIYHLLKARKSK  
EQEGFINLEMLPPELSFTILSYLNATDLCLASCVWQDLANDELLWQGLCKSTWGHCSIYNKNP  
PLGFSFRKLYMLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRTRLNWKKLRIYL  
DERRDVLDLVLTLHNFRNQFLPNALREFFRHIHAPEERGEYLETLITKFSHRFCACNPDLMRE  
LGLSPDAVYVLCYSLILLSIDLTSPhvknkmskREFIRNTRRAAQNISEDFVGHLYDNIYLI  
GVAA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 253-272

**N-glycosylation sites.**

amino acids 37-41, 87-91, 298-302

**N-myristoylation site.**

amino acids 110-116

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**FIGURE 135**

GGCACCAGGGAGCCTCCGTTAGGGGGTGGGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCA  
TCTGCTCTCTTACTGCGCAAGGGCGTAAAAAGATAGTCTTCCCATTAGCTAGAGAGCAAACCC  
CAGAAAGCCTATTGGCTGCGCCGTCGCCGGGCTTGGTCCGCTTTGAAGGCGGGCTGCGGGCTG  
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGTCGTGGTTGCTCGGAGGCACGTGTGCAGTCC  
CGGAAGCGGGCGAGGGGAAACTGCTCCGCGCGCGCGGGAGGAGGAACCGCCCGGTCTTTA  
GGGTCCGGGCCCGGCCGGGCC**ATGG**ATTCAATGCCTGAGCCCGCGTCCCGCTGTCTTCTGCTT  
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCCGCCCGGAGCTGGGCCCGAGCCAGGCC  
GGAGCTGAGGAGAACGACTGGGTTGCGCTGCCAGCAAATGCGAAGTGTGTAAATATGTTGCT  
GTGGAGCTGAAGTCAGCCTTTGAGGAAACCGGCAAGACCAAGGAGGTGATTGGCACGGGCTAT  
GGCATCCTGGACCAGAAGGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAA  
GTCACTGAGACCATTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC  
AATCGATTTGCCAAGGGCATGTGAGAGACCTTTGAGACATTACACAACCTGGTACACAAAGGG  
GTCAAGGTGGTGATGGACATCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGCTGAC  
CTCAAGAAGCAGTGTGATGTGCTGGTGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGG  
AACCACCAGGAGGAAGACCTGACTGAATTCCCTCTGCGCAACCACGTGCTGAAGGGAAAAGAC  
ACCAGTTGCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAAG  
AAGTCCAAGAAGAAGAGCAGCAGGGCCAAGGCAGCAGGCGGCAGGAGTAGCAGCAGCAAACAA  
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG  
GCATCCCCTCTCACACACAGCCCCCTGATGAGCTCT**GA**GCCCCACCCAGCATCCTCTGTCCTG  
AGACCCCTGATTTTGAAGCTGAGGAGTCAGGGGCATGGCTCTGGCAGGCCGGGATGGCCCCGC  
AGCCTTCAGCCCCCTCCTTGCTTGGCTGTGCCCTCTTCTGCCAAGGAAAGACACAAGCCCCAG  
GAAGAACTCAGAGCCGTCATGGGTAGCCACGCCGTCCTTTCCCTCCCAAGTGTTTCTCTC  
CTGACCCAGGGTTCAGGCAGCCTTGTGGTTTCAAGACTGCAAGGACTCCAGTGTGAACCTCAG  
GAGGGGCAGGTGTCAAGTGGGCACCAGGACTGGAGCCCCCTCCGGAGACCAACTCACCAT  
CCCTCAGTCTCCCCAACAGGGTACTAGGACTGCAGCCCCCTGTAGCTCCTCTCTGCTTACCC  
CTCTGTGGACACCTTGCACTCTGCCTGGCCCTTCCAGAGCCCAAAGAGTAAAAATGTTCTG  
GTTCTGATTCTGAAAAAATAAAAAAAAAAATTCTCT



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**FIGURE 136**

MDSMPEPASRCLLLPLLLLLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF  
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSGNRFAKGM  
SETFETLHNLVHKGVKVVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL  
TEFLCANHVLKGGDTSCLAEQWSGKKGDTAALGGKKSKKKSSRAKAAGGRSSSSKQKELGGL  
EGDPSPEEDEGIQKASPLTHSPPEL

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**N-glycosylation site.**

amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 227-231, 228-232

**Tyrosine kinase phosphorylation site.**

amino acids 142-150

**N-myristoylation sites.**amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,  
250-256, 263-269**Amidation sites.**

amino acids 212-216, 222-226

**ATP/GTP-binding site motif A (P-loop).**

amino acids 62-70

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**FIGURE 137**

CACGCGCTCCCGCTGCCAGCCCGGCACCGGGATCTTAATCAGTCACTATGAAAACTCATTAGCT  
CCACAGCAATGAGTCTCTCCACTGCTGAAGCTTGGCGCTGTGCTTAGTACCATGGCAATGATCT  
CAAACCTGGATGTCCCAAACCTCTCCCATCTTGGTGGGACTGAACACCACGAGGCTGTGCACTC  
CGGATACCTTAACCTCAGATTAGTCTTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC  
CTGATGGGCGGTGCATTTCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGGATGCCA  
AAAGCAGGCAACTTCGCCAACTACTGGAAAAAGGTTCAGAACATGTCCCACTCTATTGAAGTCT  
TAAACCTTGAGAACTCAGAGAGATTTCGAATATGTTTAAAAAATGGAAACCCAAATGAAAGGGC  
TGAAGGCAAAATTTCCGCAGATTGAAGATGATCGAAGACACTTATGACCAAGCATTTCAGG  
AGTTGAAGAGAAAAATGGACGAGCTCTGCCTTTGATCCCCGTGCTGGAACAGTACAAAACAG  
ATGCTAAGTTAATCACCCAGTTCAAGGAGGAATAAGGAATCTGTCTGCTGTCCTCACTGGTA  
TTCAGGAGGAAATTTGGTGCCTATGACTACGAGGAACACACCAAGAGTGCTGAGCTTGGAAA  
CAAGACTTCGTACTGCATGAAAAGCTAACATGTGGCAAACCTGATGAAAATCACAGGCCAG  
TTACAGTCAAGACATCTGGAAACCGGATTGGTGCTTGGATGACAGACCCCTTAGCATCTGAGA  
AAAACAACAGAGTCTGGTACATGGACAGTTATACTAACATAAAATTTGTCGTGAATACAAAT  
CAATTGCAGACTTTGTCACTGGGGCTGAATCAAGGACATACAACCTTCCTTTCAAGTGGGCAG  
GAACATAACCATGTTGTCTACAATGGCTCACTCTATTTTAAAGATATCAGAGTAATATCATCA  
TCAAATACAGCTTTGATATGGGAGAGTGCTTGCCCCAACGAAGCCTGGAGTATGCTGGTTTTTC  
ATAATGTTTACCCTTACACATGGGGTGGATTCTCTGACATCGACCTAATGGCTGATGAAATCG  
GGCTGTGGGCTGTGTATGCAACTAACCCAGAAATGCAGGCAATATTGTCATCAGCCAACTTAACC  
AAGATACCTTGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGGGGAAAT  
CTTTCATGATCTGTGGGACACTGTATGTCACCAACTCCCCTTAACCTGGAGCCAGGTGTATT  
ATTCCTATTTCCACCAAAACCTCCACATATGAGTACACAGACATTCCCTTCCATAACCAATAGT  
TTCACATATCCATGCTTGACTACAATGCAAGAGATCGAGCTCTCTATGCTTGGAAACATGGCC  
ACCAGGTGCTGTTCAATGTCACCCCTTTTCCATATCATCAAGACAGAGGATGACACATAGCGAA  
ATGTGACATGTTTTTATTGATTTAAACAGTGTGATTGTGATAAACTCTATAAGACCCCTTCC  
GTTTTTTTCTTCACTATTATTTTTCATATTCTCCAAAGCAAAGCATTTTTATTGTAAAGTT  
GGTGTTCAAAAACATAGCTGAGCTTGCTCTAACTTACCATGTTGGAAACACATCTTAACTTCT  
AAATTTACAAGGCCTATCATGTCTTGTATGAAAAGCACTAAAAAAGAGGTTTAAAGT  
GGCTAAAGTCATAGTTTGAAGAGATTAAATGATCTGCCTTATATTAGAGTCAGAGACTAATG  
GTGGCTTAAATGCACGAATGTCTTTTTTTTTTAAACTGTCAATTTTTACTGTCTTTTGCTCCA  
TCTCAGGAAATATTTTGGTAGGAATTAGGAGAACAAAAAGCACTTTTATCCCATTTTATTCTT  
TAAAAAATGTAAGGATTTTCATTTTATATTGAAAAATAATATTAATCATTTTGCTGTTAACACAA  
TTCTCTGATCGGGTGTCTAGCACTCATTTTTTAAATCTCTGCTAACATTTTATTGGCAGTATG  
TATTTCTACCATTTGTAACCACTTGTGCTATTGTATCTCTTCACTTCTGTGAAAGTAATATT  
TTTATATAAANACACTGNAATTTTAAAAAAGAAAAAAGCAAAAAAAGAAAAAAGAAAAA